GenCore version 5.1.4\_p5\_4578 Copyright (c) 1993 - 2003 Compugen Ltd.

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Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Total number of hits satisfying chosen parameters:
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Maximum DB seq length: 2000000000
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2681
1 MFETEHHTLLPLLLL
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1: /SIDS2/gcgdata/g
2: /SIDS2/gcgdata/g
3: /SIDS2/gcgdata/g
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1020.262 million cell updates/sec
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

## SUMMARI

10087654		Result No.
978.5 978.5 978.5 978.5 946 946 816.5	2681 978.5	Score
35.35.55.55.55.55.55.55.55.55.55.55.55.5	100.0	Query Match Length DB
47/2 491 492 444 444 486	513 472	ength [
221 221 221 221 221 221 221 221 221 221	18	В
AAC45022 AAG45021 AAG45021 AAG44570 AAG44572 AAG44572 AAG45023 AAB91571 AAU02839	AAB07921 AAW27153	ID
Arabidopsis thalia	A cytochrome P450 Arabidopsis thalia	Description

PT DR XX

Azpiroz R, Choe S, WPI; 2000-549142/50. N-PSDB; AAA59599.

Feldmann KA;

New isolated dwf4 polynucleotide useful for altering the phenotype of plants, for diagnostic assays and in the production of antibodies -

		•							_	•																								
<b>4</b> 51	44	43	42	41	40	39	38	37	36	35 .	34	33	32	31	30	29	28	27	26	25	24	23	22	21	20	19	18	17	16	15	14	13	12	11
461	490	503	503	503	503	528.5	534.5	546	547.5	553.5	558.5	558.5	564	564	568.5	569.5	571	583	585	588	592	596.5	597.5	598.5	603	606	606	653.5	712	712	712	726	726	726
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497	433	492	492	492	492	388	503	481	489	498	512	483	500	484	500	493	501	484	507	509	496	497	485	430	469	479	471	468	465	462	461	465	462	461
19	21	23	22	19	19	21	22	21	21	22	22	22	22	22	22	22	22	22	22	22	22	22	22	21	21	21	21	21	21	21	21	21	21	21
AAW37735	AAG30050	AAE15325	AAB85155	AAW44159	AAW37733	AAG20785	AAU02828	AAG30049	AAG30048	AAU02838	AAU02834	AAU02827	AAU02826	AAU02821	AAU02824	AAU02836	AAU02823	AAU02822	AAU02830	AAU02832	AAU02837	AAU02829	AAU02835	AAG20784	AAG23014	AAG23012	AAG23013	AAG20783	AAG11834	AAG11835	AAG11836	AAG46491	AAG46489	AAG46490
יסי	Arabidopsis thalia	Zebrafish P450RAI	Zebrafish cytochro	Zebrafish retinoid	Cytochrome zP450RA	Arabidopsis thalia	data	tha	dopsis thal	cuspidata	cuspidata	cuspidata	cuspidata		cuspidata	cuspidata	cuspidata	cuspidata	cuspidata				ď						S		8	15	18	Arabidopsis thalia

## ALIGNMENTS

RESULT 1

AAB07921	7921
ij	AAB07921 standard; Protein; 513 AA.
×	
AC	AAB07921;
×	
ΔŢ	14-NOV-2000 (first entry)
×	
DE	A cytochrome P450 enzyme designated DWF4.
X	
X	DWF4; cytochrome P450 enzyme; brassinosteroid; 22alpha-hydroxylation;
X	plant phenotype; cell elongation.
XX	
80	Arabidopsis sp.
X	
PN	WO200047715-A2.
XX	
PD	17-AUG-2000.
×	
ΡF	11-FEB-2000; 2000WO-US03820.
×	
PR	11-FEB-1999; 99US-0119657.
PR	11-FEB-1999; 99US-0119658.
×	
PA	(ARIZ-) ARIZONA BOARD OF REGENTS.
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Matches 513
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                                                                                                    Cytochrome P450-type hydroxylase; idbrassinosteroid inhibitor; modified
                         Arabidopsis thaliana
                                                                                                                                                                                                                                            14-APR-1998
                                                                                                                                                                                                                                                                                                                                                AAW27153 standard;
                                                                                                                                                                                  Arabidopsis thaliana cytochrome P450-type hydroxylase.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                YKKMDFTQCVINETLRLGNVVRFLHRKALKDVRYKGYDIPSGWKVLPVISAVHLDNSRYD
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 YKKMDFTQCVINETLRLGNVVRFLHRKALKDVRYKGYDIPSGWKVLPVISAVHLDNSRYD
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ILDLILSLLFAGHETSSVAIALAIFFLQACPKAVEELREEHLEIARAKKELGESELNWDD
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13; Conservative
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                                                                                                                                                                                                                                    (first entry)
                                                                                                                                                                                                                                                                                                                                                   Protein; 472
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Pred. No. 1.3e-228;
D; Mismatches 0;
                                                                                                                                                                                                                                                                                                                                                   ₿
                                                                                                                                identification; brassinosteroid;
                                                                                                    plant;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     513
                                                                                                    recombinant production;
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Matches 210;
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Best Local
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          The present sequence is Arabidopsis thaliana cytochrome p450-type hydroxylase. The hydroxylase can be used to identify brassinosteroids or brassinosteroid inhibitors, useful to produce
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      New isolated plant cytochrome P450-type hydroxylase gene - used to identify substances acting as brassino-steroid(s) or brassinosteroid inhibitors for the production of modified plants
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                                                                                                                                                                                                                                                                                    GHETSSVATALAIFFLQACPKAVEELREEHLEIARAKKELGESELNWDDYKKMDFTQCVI
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                                                      QQNNGASSSGSGSFSTWGNN-YMPFGGGPRLCAGSELAKLEMAVFIHHLVLKFNWELAED
                                                                                                               NETLRVANIIGGVFRRAMTDVEIKGYKIPKGWKVFSSFRAVHLDPNHFKDARTFNPWRWQ
                                                                                                                                                                                                                              GYETTSTIMTLAVKFLTETPLALAQLKEEHEKIRAMKSD--SYSLEWSDYKSMPFTQCVV
                                                                                                                                                                                                                                                                                                                                                 VVVMKRREEEEEGAE------RKKDMLAALLAADDGFSDEEIVDFLVALLVA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                LMSFDPG-EWSESLRKEYLLVIEGFFSLPLPLFSTTYRKAIQAR-----RKVAEALT
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SNSVTTGPSNVFTPFGGGPRLCPGYELARVALSVFLHRLVTGFSWVPAEQ
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Pred. No. 6.6e-78;
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netic mapping; gene expression control; promoter;
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Query Match 36.5%;
Best Local Similarity 41.9%;
Matches 210; Conservative 7
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                                                                                                                                                                                                                                                                                                                                                                                                                  Arabidopsis thaliana protein fragment
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41.9%; Pred. No. 7e-78;
tive 79; Mismatches 171;
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06-APR-1999

08-APR-1999
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28-OCT-1999
                    06-SEP-2000
                                                                                Protein identification; signal transduction pathway; metabolic pathway; hybridisation assay; genetic mapping; gene expression control; promoter;
                                                                                                                                                                  AAG45023
  25-FEB-2000; 2000EP-0301439
                                       EP1033405-A2
                                                       Arabidopsis thaliana
                                                                          termination
                                                                                                           Arabidopsis thaliana protein fragment SEQ ID NO: 56470.
                                                                                                                               18-OCT-2000
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                                                                                                                                                                                                                                                                                                                                                                        APLNLPGTAYHKALQSRATILKFIERKMEERKLDIKEEDQEEEEVKTEDEAEMSKSDHVR
                                                                                                                                                                                                                                                                                                                                                                                                         RHTLFVLDSWQQNSIFSAQDEAKKFTFNLMAKHIMSMDPGEEETEQLKKEYVTFMKGVVS
                                                                                                                                                                                                                                                                                                                                                                                                                                   FVLQNEGKLFECSYPASICNLLGKHSLLLMKGSLHKRMHSLTMSFANSSIIKDHLMLDID
                                                                                                                                                                                                                                                                                                                                                                                                                                             FILQNEGRLFECSYPRSIGGILGKWSMLVLVGDMHRDMRSISLNFLSHARLRTILLKDVE
                                                                                                                                                                                                                                                                                                                                                                                                RLVRFNLDSWSSRVLL--MEEAKKITFELTVKQLMSFDPG-EWSESLRKEYLLVIEGFFS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           198;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Similarity
                                                                                                                                                                 standard; Protein; 444
                                                                        sequence
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990S-0160980
990S-0160989
990S-0161404
990S-0161406
990S-0161406
990S-0161359
990S-0161361
990S-0161361
990S-0161361
990S-0161920
990S-0161920
990S-0161920
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Pred. No. 4.6e-75;
7; Mismatches 161;
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30-APR 1999
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06-MAY 1999
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11-MAY 1999
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05-MAR-1999
09-MAR-1999
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16-APR-1999
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18-JUN-1999;
18-JUN-1999;
18-JUN-1999;
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18-JUN-1999;
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Best Local Similarity
Matches 198; Conserv
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                                        FILQNEGRLFECSYPRSIGGILGKWSMLVLVGDMHRDMRSISLNFLSHARLRTILLKDVE
                                                                                                                                                                                                                 RHTLFVLDSWQQNSIFSAQDEAKKFTFNLMAKHIMSMDPGEEETEQLKKEYVTFMKGVVS
                                                                                                                                                                                                      RLVRFNLDSWSSRVLL--MEEAKKITFELTVKQLMSFDPG-EWSESLRKEYLLVIEGFFS
                                                                                                                                                                                                                                              FVLQNEGKLFECSYPASICNLLGKHSLLLMKGSLHKRMHSLTMSFANSSIIKDHLMLDID
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990S-0159637

990S-0159638

990S-0160741

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990S-0160768

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990S-0160815

990S-0160815

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99US-0157117.
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Pred. No. 4.6e-
77; Mismatches
                                                                                                                                                                                                                                                                                                                                       946; DB 21;
No. 4.6e-75;
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990S-014433.
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990S-014508.
990S-014720.
990S-014723.
990S-014723.
990S-0151303.
990S-0152363.
990S-01524018.
990S-0155139.
990S-0155659.
990S-0155659.

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RESULT 9
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                                                                                                                                                                                                                                                                                                                                                                                           The invention relates to identifying target proteins (ABB90790-ABB94016) for herbicidally active compounds, comprising alighing and comparing nucleic acid or amino acid sequences from plant with nucleic acid or amino acid sequences from non-plant organisms using suitable search parameters, where plant sequences having an E-value greater by a factor of 3 than the E-value of most similar non-plant sequences are selected. The polypeptides or nucleic acids encoding them are useful for identifying modulators. The identified modulators are
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Claim
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Identifying plant target proteins for herbicidally active compounds, comprising aligning and comparing nucleic acid or amino acid sequence from plant with nucleic acid or amino acid sequences from non-plant
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             WPI;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           07-FEB-2002
                                                                                                                                                                                                                                                                                                                                                         Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           organisms -
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Tietjen
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         28-AUG-2001; 2001WO-EP09892
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2002-269010/31
                                                             NLPGTAYHKALQSRATILKFIERKMEERKLDIKEEDQEEEEVKTEDEAEMSKSDHVRKQR
                                                                                                                 LFVLDSWQQNSIFSAQDEAKKFTFNLMAKHIMSMDPGEEETEQLKKEYVTFMKGVVSAPL
                                                                                                                                             QNEGKLFQSSYPKSFRDLVGKDGVITVHGDQQRRLHSIASSMMRHDQLKTHFLEVIPVVM
                                                                                                                                                                     QNEGRLFECSYPRSIGGILGKWSMLVLVGDMHRDMRSISLNFLSHARLRTILLKDVERHT
                                                                                                                                                                                               FVEKQIKKFVSLLCSVLLLILKRPDNSGFNEIRYGRIFSCSLFGKWAVVSADPDFNRFIM
                                                                                                                                                                                                                                                  LLSVSSSTTFLAFIIIFLLAGIARRKRRAPHRLPPGSRGWPLIGDTFAWLNAVAGSHPSS
                                       DLPGFTYNKAMKARKEIIRKINKTIEKRLQNKAASD------
                                                                                         LQTLSNFKDGEVVLLQDICRKVAIHLMVNQLLGVS-SESEVDEMSQLFSDFVDGCLSVPI
                                                                                                                                                                                                                                                                                                      181;
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                                                                                                                                                                                                                                                                                                                 32.3%;
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                                                                                                                                                                                                                                                                                                    Score 866; DB 23;
Pred. No. 6.8e-68;
5; Mismatches 173;
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LFICVILLLLRRSNDRQGNGSANKPKLPPGSAGLPFIGETIRFLRDAKSPGRRKFFDEHE

LSLLLFLILLKRRNRK-----TRENLPPGKSGWPFLGETIGYLKPYTATTLGDFMQQHV 72

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19 20

Best Matches Query Match

hes 176;

Similarity

30.5%;

Score 816.5; DB 2 Pred. No. 1.5e-63;

DB 22; 184;

Conservative

97;

Mismatches

Indels Length 486;

45;

Gaps

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Sequence

486

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RESULT 10
AAU02839
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                                                                  The sequence represents a Taxus cuspidata oxygenase, encoded by a DNA of the invention. The sequences isolated from the Taxus genus, and the respective oxygenases are useful for the synthetic production of Taxol and related taxoids, as well as intermediates within the Taxol biosynthetic pathway, and other taxoid derivatives. The sequences also can be used to make transgenic oxygenases that either produce the oxygenases for subsequent in vitro use, or produce the oxygenases in vives so as to alter the produce of Taxol and taxoid production within the transgenic oxygenases to alter the produce the oxygenases.
                        transgenic organism. The oxygenase nucleic acids and amino acids are useful for isolating the polynucleotide and polypeptide sequences corresponding to full-length oxygenases.
                                                                                                                                                                                                                                                                         Novel nucleic acid and amino acid sequences, isolated from the Taxus genus, useful for the synthetic production of Taxol and related
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Taxus cuspidata
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                                                                                                                                                                                                                Claim 1;
                                                                                                                                                                                                                                            taxoids, intermediates within other taxoid derivatives -
                                                                                                                                                                                                                                                                                                                        N-PSDB; AAS05196.
                                                                                                                                                                                                                                                                                                                                                                       Croteau
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RESULT 11
AAG46490
ID AAG46
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05-MAR-1999
09-MAR-1999
23-MAR-1999
25-MAR-1999
01-APR-1999
01-APR-1999
16-APR-1999
16-APR-1999
21-APR-1999
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9908-0123180
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RESULT 12
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Best Local Similarity 32.3%;
Matches 166; Conservative
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28-OCT-1999;
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                                 Protein identification; signal transduction pathway; metabolic hybridisation assay; genetic mapping; gene expression control;
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                                                                                                                                                                                                                 standard; Protein; 462
                                                                                             thaliana protein fragment SEQ ID NO: 58493.
                    sequence
                                                                                                                                      (first entry)
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990S-0161404.
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; Pred. No. 1.5e-55;
91; Mismatches 181;
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promoter;
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05-CCT-1999
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4-OCT-1999;
                                                                                                                                                                                                        LLLLPSLLSLLLFLILLKRRN--RKTRFNLPPGKSGWPFLGETIGYLKPYTATTLGDFMQ
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 FIERKMEERKLDIKEEDQEEEEVKTEDEAEMSKSDHVRKQRTDDDLLGWVLKHSN----L
                                                                                                                                                               LLIIVSLCSALL-----
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                                                                                                                       TQIAGNLRKPFV-----
                                                                                                                                           ----NLMAKHIMSMDPGEEETEQLKKEYVTFMKGVVSAPLNLPGTAYHKALQSRATILK
                                                                                                                                                                                                                                                                                                           Similarity
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99US-0158029

99US-0158232

99US-0159294

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S-0157117.
S-0157753.
S-0157865.
S-0158029.
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                                                                                                                                                                                                                                                                                              score 726; DBPred. No. 1.5e91; Mismatches
                                                                                                                     -EEFKTAFFKLVVGTLSVPIDLPGTNYRCGIQARNNIDR
                                                                            DSGE---
                                                                                                                                                                                                                                                                                               DB 21; 1
|.5e-55;
|es 181;
                                                                            -TFTDMLGYLMKKEGNRYPL
                                                                                                                                                                                                                                                                                                                    Length 462;
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30-APR-1999;
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23-APR-1999;
23-APR-1999;
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05-MAR-1999;
09-MAR-1999;
23-MAR-1999;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Protein identification; signal transduction pathway; metabolic pathway; hybridisation assay; genetic mapping; gene expression control; promoter;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         18-OCT-2000
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01-APR-1999;
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                                                                                                                                                                                                                                                                         28-APR-1999;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        termination
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99US-0130077.
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99US-0130510.
99US-0130891.
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99US-0128234.
99US-0128714.
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99US-0123180
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18-OCT-1999
             y Match 27.1%;
Local Similarity 32.3%;
hes 166; Conservative
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             Score 726; DB Pred. No. 1.5e-91; Mismatches
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             Gaps
69
              10;
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118-JU

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RESULT 14

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23-MAR-1999

25-MAR-1999

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23-APR-1999
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                                                                                                                                                                                                                                                                                                                                   Arabidopsis thaliana.
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Protein identification; signal transduction pathway; metabolic hybridisation assay; genetic mapping; gene expression control;
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                                                          KLDIKEEDQEEEEVKTEDEAEMSKSDHVRKQRTDDDLLGWVLKHSN----LSTEQILDLI 305
                                                                                            KHIMSMDPGEEETEQLKKEYYTFMKGVVSAPLNLPGTAYHKALQSRATILKFIERKMEER 249
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Search completed: March 30, Job time: 69 secs 2003, 12:04:18 멍

436

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                Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.
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1: /cgn2_6/ptodata/1,
2: /cgn2_6/ptodata/1,
3: /cgn2_6/ptodata/1,
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/cgn2_6/ptodata/1/iaa/BCTUS_COMB.pep:*
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US-08-724-466B-4
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Query Match 36.5%; Score 978.5; DB 2; Length 472; Best Local Similarity 41.9%; Pred. No. 5e-89; Matches 210; Conservative 79; Mismatches 171; Indels 41; Gaps 8;	US-08-622-166A-2 US-08-622-166A US-08-622-166A Patent No. 595245 Patent No. 595245 PAPLICANT: MATHUR, JAIDEEP APPLICANT: STERERS, MIKLOS APPLICANT: MATHUR, JAIDEEP APPLICANT: MATHUR, JAIDEEP APPLICANT: MICHANIN, THOMAS TITLE OF INVENTION: MICHEIC ACID MOLECULES ENCODING CYTOCHROME TITLE OF INVENTION: MICHEIC ACID MOLECULES TITLE OF INVENTION: MICHEIC ACID MOLECULES TITLE OF INVENTION ACID MICHEIC ACID MOLECULES TOPOLOXET MICHEIC TORN TELEPHONE: (703) 205-8050 TELEPHONE: (703) 205-8050 TELEPHONE: CHARACTERISTICS: LENGTH: 472 maino acid TYPE: MICHEIC TYPE: DIOTEIN US-08-622-166A-2	28 242.5 9.0 502 4 US-09-499-302A-4 29 241.5 9.0 531 4 US-09-380-420C-2 30 241 9.0 490 4 US-09-126-420A-16 31 241 9.0 510 3 US-09-166-505B-66 32 241 9.0 510 3 US-08-616-90-66 Sequence 16, Appl 33 240.5 9.0 509 3 US-08-948-564-18 34 239 8.9 496 1 US-08-313-075A-50 35 236 8.8 521 30-6948-564-14 Sequence 18, Appl 36 234.5 8.7 490 1 US-08-21B-1 37 234.5 8.7 490 2 US-08-238-821B-1 38 234.5 8.7 508 4 US-08-238-821B-1 39 233.5 8.7 508 4 US-08-238-821B-1 39 233.5 8.7 508 4 US-08-313-075A-3 40 232.5 8.7 508 4 US-08-91-677-2 40 232.5 8.7 504 4 US-08-313-075A-38 42 231 8.6 506 1 US-08-313-075A-38 43 231 8.6 506 1 US-08-313-075A-38 44 225.5 8.4 471 4 US-09-126-420A-20  ALIGNMENTS  ALIGNMENTS

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RESULT 2
US-08-622-166A-4
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                      INFORMATION FOR SEQ ID NO:
                                                                                                                                                                                           COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTMARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/622,166A
FILING DATE: 27-MAR-1996
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          APPLICANT:
APPLICANT:
APPLICANT:
                                                                                       REGISTRATION NUMBER: 30,330
REFERENCE/DOCKET NUMBER: 01-
TELECOMMUNICATION INFORMATION:
                                                                                                                                                             CLASSIFICATION: 800
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                     NUMBER OF SEQUENCES: 4
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          TITLE OF INVENTION:
     SEQUENCE
                         TELEFAX: 1/2
TELEFAX: 248345
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                              ESSEE: Birch, Ste
ET: P.O. Box 747
: Falls Church
                                                                                                                                                                                                                                                                                                                                               22040-0747
                                                                                                                                                                                                                                                                                                                                                            Virginia
Y: USA
                                                                                                                                                SVENSSON, LEONARD R.
     CHARACTERISTICS:
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SZEKERES, MIKLOS
ALTMANN, THOMAS
                                                       (703) 205-8050
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                                                                            (703)
                                                                        205-8000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         NUCLEIC ACID MOLECULES ENCODING CYTOCHROME P450-TYPE PROTEINS INVOLVED IN THE BRASSIN
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Best Local S
Matches 210
                                                                                                                                                                                                                                                                                                                                                                           Sequence 2, Application US/08724466B Patent No. 6063606 GENERAL INFORMATION:
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TOPOLOGY: linear
MOLECULE TYPE: prot
                                 CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/72/
FILING DATE: October 1, 1996
PRIOR APPLICATION DATA:
                                                                                                                                                                              COMPUTER READABLE FORM
                                                                                                                                                                                                                                                                   CORRESPONDENCE ADDRESS:
ADDRESSEE: Blake, Ca
                                                                                                                                                                                                                                                                                                                       APPLICANT: Petkovich, P. Martin, White, Jay A., APPLICANT: Beckett, Barbara R., Jones, Glenville TITLE OF INVENTION: Retinoid Metabolizing Protein
                                                                                                                                                                                                                                                                                                        NUMBER OF SEQUENCES:
                                                                                                COMPUTER: COMPAQ, IBM PC OPERATING SYSTEM: MS-DOS SOFTMARE: WORD DEBEN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         447
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                                                                                                                                                                                                  ZIP: M5L 1A9
COUNTRY: Canada
                APPLICATION NUMBER:
                                                                                                                                                                                                                                                    STREET:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        64 VARYGSVFMTHLFGEPTIFSADPETNRFVLQNEGKLFECSYPASICNLLGKHSLLLMKGS 123
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         72 VSKYGKIYRSNLFGEPTIVSADAGLNRFILQNEGRLFECSYPRSIGGILGKWSMLVLVGD 131
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                QQNNGASSSGSGSFSTWGNN-YMPFGGGPRLCAGSELAKLEMAVFIHHLVLKFNWELAED 490
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                                                                                                                                                                                                                                Toronto
                                                                                                                                                                                                                                                    Box 25,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Conservative
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June 21,
                                                                                                                                                                                                                                                      Commerce
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  36.5%; Score 978.5;
41.9%; Pred. No. 5e
                                                                                                                                                                                                                                                                   Cassels & Graydon
                                                                                                                                                                                                                                                                                                        30
   08/667,546
1, 1996
                                                                      US/08/724,466B
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          -----RKKDMLAALLAADDGFSDEEIVDFLVALLVA 278
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 79; Mismatches 171;
                                                                                                                          compatible 5.1
                                                                                                                                                           1/2 inch,
                                                                                                                                                                                                                                                    Court
                                                                                                                                                                                                                                                      West
                                                                                                                                                             1.4 Mb storage
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5e-89;
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RESULT 4
US-08-882-164D-2
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                                                                                                                                                                                                                                                                                    Sequence 2, Application US/08882164D Patent No. 6306624 GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Matches 144; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               TELEFAX: (416) 863-2653
INFORMATION FOR SEQ ID NO: 2:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       REFERENCE/DOCKET NUMBER: 50
TELECOMMUNICATION INFORMATION:
TELEPHONE: (416) 863-4344
                                                                                                                                                           APPLICANT: Petkovich, P. Martin, White, Jay A., APPLICANT: Beckett, Barbara R., Jones, Glenville TITLE OF INVENTION: Retinoid Metabolizing Protein NUMBER OF SEQUENCES: 43
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ATTORNEY/AGENT INFORMATION:
NAME: Hunt, John C.
  COMPUTER READABLE FORM:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   407
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   351
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          TYPE: amino acid
STRANDEDNESS: single
                                                 COUNTRY:
                                                                            STATE:
                                                                                                                      STREET:
                                                                                                                                              ADDRESSEE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     4 YTLMVTFLCTIVLPVLLFLAAVKLWEMLMIRRVDPNCRSPLPPGTMGLPFIGETLQLI--
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Match 18.8%;
Local Similarity 27.6%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            TOPOLOGY:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      LKHSNLSTEQILDLILSLLFAGHETSSVAIALAIFFLQACPKAVEELREEHLEIARAKKE 350
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     LAKLEMAVFIHHLVLKFNWELAEDDQ-----PFAFPFVDFP 502
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                PVISAVHLDNSRYDQPNLFNPWRWQQQNNGASSSGSGSFSTWGNNYMPFGGGPRLCAGSE 466
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            LG----ESELNWDDYKKMDFTQCVINETLRLGNVVRFLHRKALKDVRYKGYDIPSGWKVL 406
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              CVLVYPEMKKLMFRIAMRILLGFEPEQIKTDEQELVEAFEEMIKNLFSLPIDVPFSGLYR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ILGKWSMLVLVGDMHRD-----MRSISLNFLSHARLRTILLKDVERHTLFVLDSW-QQNS 172
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ---LQRRKFLRMKRQKYGCIYKTHLFGNPTVRVMGADNVRQILLGEHKLVSVQWPASVRT 118
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      YTATTLGDFMQQHVSKYGKIYRSNLFGEPTIVSADAGLNRFILQNEGRLFECSYPRSIGG 118
                                                                                                                                                                                                                                                                                                                                                                                                                                                      FAKVLLKIFLVELTQHCNWILSNGPPTMKTGPTIYPVDNLP 483
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    YSICDTHDVADVFPNKEEFQPERFM----
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ----PFSLQAMKEAATELLFGGHETTASTATSLVMFLGLNTEVVQKVREE----VQEKVE 331
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        GLRAR----IENSRIEENIRKKIQDDDNENEQKYKDALQLL----IENSRRSDE----
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             IFSAQDEAKKFTFNLMAKHIMSMDPGEEET -- EQLKKEYVTFMKGVVSAPLNLPGTAYHK 230
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ILGSDTLSNVHGVQHKNKKKAIMRAFSRDALEH-----YIPVIQQEVKSAIQEWLQKDS 172
                                                                     Toronto
: Ontario
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M5L 1A9
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                                                                                                                      Box 25,
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                   RESULT 5
US-08-802-164D-32
; Sequence 32, Application US/08882164D
; Patent No. 6306624
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Best Local :
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GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         TELEFAX: (416) 863-2653 INFORMATION FOR SEQ ID NO: 2: SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           REFERENCE/DOCKET NUMBER: 50
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION 105084344
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   APPLICATION NUMBER: US/08/882,164D FILING DATE: June 25, 1997 PRIOR APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ATTORNEY/AGENT INFORMATION:
NAME: Hunt, John C.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           CURRENT APPLICATION DATA:
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                                                                                                                                                                                                                                                                                                          407
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                                                                                                                                                                                                                                                                392
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         231 ALQSRATILKFIERKMEERKLDIKEEDQEEEEVKTEDEAEMSKSDHVRKQRTDDDLLGWV
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     APPLICATION NUMBER: 08/667,546
FILING DATE: June 21, 1996
APPLICATION NUMBER: 08/724,466
FILING DATE: October 1, 1996
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           MEDIUM TYPE: Diskette, 3 1/2 inch, COMPOTER: COMPAQ, IBM PC compatible OPERATING SYSTEM: MS-DOS 5.1 SOFTWARF. WORD TO SOFTWARF.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                TOPOLOGY: 11
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   62 ----LQRRKFLRMKRQKYGCIYKTHLFGNPTVRVMGADNVRQILLGEHKLVSVQWPASVRT 118
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                59 YTATTLGDFMQQHVSKYGKIYRSNLFGEPTIVSADAGLNRFILQNEGRLFECSYPRSIGG 118
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Match 18.8%;
Local Similarity 27.6%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            TYPE: amino acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                REGISTRATION NUMBER: 36,424
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             7 HTLLPLLLLPSLLSLLLFL------ILLKRRNRKTRFNLPPGKSGWPFLGETIGYLKP 58
                                                                                                                                                                                                            LAKLEMAVFIHHLVLKFNWELAEDDQ-----PFAFPFVDFP 502
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              YTLMVTFLCTIVLPVLLFLAAVKLWEMLMIRRVDPNCRSPLPPGTMGLPFIGETLQLI-- 61
                                                                                                                                                                                                                                                                                                                                                                                                                                                 ----PFSLQAMKEAATELLFGGHETTASTATSLVMFLGLNTEVVQKVREE----VQEKVE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               GLRAR----IENSRIEENIRKKIQDDDNENEQKYKDALQLL----IENSRRSDE-----
                                                                                                                                                                                                                                                                                                                                                                                                LG----ESELNWDDYKKMDFTQCVINETLRLGNVVRFLHRKALKDVRYKGYDIPSGWKVL 406
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              LKHSNLSTEQILDLILSLLFAGHETSSVAIALAIFFLQACPKAVEELREEHLEIARAKKE
                                                                                                                                                                                                                                                           YSICDTHDVADVFPNKEEFQPERFM-----SKGLEDGSRF--NYIPFGGGSRMCVGKE 442
                                                                                                                                                                                                                                                                                                       PVISAVHLDNSRYDQPNLENPWRWQQQNNGASSSGSGSFSTWGNNYMPFGGGPRLCAGSE
                                                                                                                                                                                                                                                                                                                                                         MGMYTPGKGLSMELLDQLKYTGCVIKETLRINPPVPGGFRVALKTFELNGYQIPKGWNVI 391
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       IFSAQDEAKKETFNLMAKHIMSMDPGEEET--EQLKKEYVTFMKGVVSAPLNLPGTAYHK 230
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ILGSDTLSNVHGVQHKNKKKAIMRAFSRDALEH-----YIPVIQQEVKSAIQEWLQKDS
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US-08-882-164D-32
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Best Local Simi
Matches 148;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           TELEFAX: (416) 863-265
INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/667,546
FILING DATE: June 21, 1996
APPLICATION NUMBER: 08/724,466
FILING DATE: October 1, 1996
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/
FILING DATE: June 25, 1997
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   NAME: Hunt, John C.
REGISTATION NUMBER: 36,424
REFERENCE/DOCKET NUMBER: 50
TELECOMMUNICATION INFORMATION:
TELEPHONE: (416) 863-4344
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 COMPUTER READABLE FORM:

MEDIUM TYPE: Diskette, 3 1/2 inch, 1
COMPUTER: COMPAQ, IBM PC compatible
OPERATING SYSTEM: MS-DOS 5.1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      APPLICANT: Petkovich, P. Martin, White, Jay A., APPLICANT: Beckett, Barbara R., Jones, Glenville TITLE OF INVENTION: Retinoid Metabolizing Protein
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CORRESPONDENCE ADDRESS:
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TOPOLOGY: Li
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PVISAVHLDNSRYDQPNLENPWRWQQQNNGASSSGSGSFSTWGNNYMPFGGGPRLCAGSE
                                                          LCKSNQDNKLDMETLEQLKYIGCVIKETLRLNPPVPGGFRVALKTFELNGYQIPKGWNVI 395
                                                                                      AKKELGESELNWDDYKKMDFTQCVINETLRLGNVVRFLHRKALKDVRYKGYDIPSGWKVL
                                                                                                                                                                                                                             VKARNLIHARIEENIRAKIRRLQATEPDGGCKDALQLLIEHSWE-----RGERLDMQ-
                                                                                                                                                                                                                                                                                                                 VYPEVKRLMFRIAMRILLGCEPGPAGGGEDEQQLVEAFEEMTRNLFSLPIDVPFSGLYRG
                                                                                                                                                                                                                                                                                                                                                      AQDEAKKFTFNLMAKHIMSMDPGE----EETEQLKKEYVTFMKGVVSAPLNLPGTAYHKA 231
                                                                                                                                                                                                                                                                                                                                                                                                  TILGAGCLSNLHDSSHKQRKKVIMQAFSREALQCYVLV-IAEEVSSCLEQWLSCGERGLL 176
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    LPALLASALCTFVLPLLLFLAALKLWDLYCVSSRDRSCALPLPPGTMGFPFFGETL----
                                                                                                                                                 ---ALKQS--STE-----
                                                                                                                                                                                    LGWVLKHSNLSTEQILDLILSLLFAGHETSSVAIALAIFFLQACPKAVEELREEHLEIAR
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  -QMVLQRRKFLQMKRRKYGFIYKTHLFGRPTVRVMGADNVRRILLGEHRLVSVHWPASVR 117
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1: Canada
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Best Local (
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       APPLICATION NUMBER: 08/667.54
ETILING DATE: June 21, 1996
ATTORNEY/AGENT INFORMATION:
NAME: Hunt, John C.
REGISTRATION NUMBER: 36,424
REFERENCE/DOCKET NUMBER: 5076
TELECOMMUNICATION INFORMATION:
TELEPHONE: (416) 863-4344
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    TELEFAX: (416) 863-2653 INFORMATION FOR SEQ ID NO:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               SEQUENCE CHARACTERISTICS:
LENGTH: 497 amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    PRIOR APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette, 3 1/2 inch, 1
COMPUTER: COMPAQ, IBM PC compatible
OPERATING SYSTEM: MS-DOS 5.1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      APPLICANT: Petkovich, P. Martin, White, Jay A., APPLICANT: Beckett, Barbara R., Jones, Glenville TITLE OF INVENTION: Retinoid Metabolizing Protein
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CORRESPONDENCE ADDRESS:
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                                                                                                                    174 GLLVYPEVKRLMFRIAMRILLGCEPQLAGDGDSE-QQLVEAFEEMTRNLFSLPIDVPFSG
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DDDLLGWVLKHSNLSTEQILDLILSLLFAGHETSSVAIALAIFFLQACPKAVEELREEHL
                                    LYRGMKARNLIHARIEQNIRAKICGLRASEAGQGCKDALQLLIEHSWE-----RGERL
                                                                           YHKALQSRATILKFIERKMEERKLDIKEED-----QEEEEVKTEDEAEMSKSDHVRKQRT 282
                                                                                                                                                                                                TILGSGCLSNLHDSSHKORKKVIMRAFSREALECYVPVITEEVGSS----LEQWLSCGER 173
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                                                                                                                                                         IFSAQDEAKKETENLMAKHIMSMDP-----GEEETEQLKKEYVTEMKGVVSAPLNLPGTA 227
                                                                                                                                                                                                                                                                              -QMVLQRRKFLQMKRRKYGFIYKTHLFGRPTVRVMGADNVRRILLGDDRLVSVHWPASVR 117
                                                                                                                                                                                                                                                                                                                   PYTATTLGDFMQQHVSKYGKIYRSNLFGEPTIVSADAGLNRFILQNEGRLFECSYPRSIG 117
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'RY: Canada
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                                                                                                                                                                                                                                                                                                                                                                                                                                     85; M1smatches 226;
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US-08-882-164D-4
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                                                                                                                                                                                                                                                                                                       SEQUENCE CHARACTERISTICS:
LENGTH: 497 amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       APPLICATION NUMBER: US/08/
FILING DATE: June 25, 1997
PRIOR APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              SOFTWARE: WORD PERFECT CURRENT APPLICATION DATA:
118 GILGKWSMLVLVGDMHRDMRSISLNFLSHARLR---TILLKDVERHTLFVLDSWQQ--NS
                                                                                                                                                                                                                                                                                                                                                                                          TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                           ATTORNEY/AGENT INFORMATION:
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NUMBER OF SEQUENCES:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          APPLICANT: Petkovich, P. Martin, White, Jay A., APPLICANT: Beckett, Barbara R., Jones, Glenville TITLE OF INVENTION: Retinoid Metabolizing Protein
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                                                                                                                              10 LPLLLLPSL----LSLLLFLILLK-----RRNRKTRFNLPPGKSGWPFLGETIGYLK 57
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                                                                                                                                                                                            Local Similarity
                                                                                                                                                                                                                                                           TOPOLOGY: 11
                                                                                                                                                                                                                                                                                             TYPE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                             APPLICATION NUMBER: 08/667,546
FILING DATE: June 21, 1996
APPLICATION NUMBER: 08/724,466
FILING DATE: October 1, 1996
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                                                                                                                                                                                                                                                                                                                                                                                                                    NAME: Hunt, John C.
REGISTRATION NUMBER: 36,424
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          OPERATING SYSTEM:
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                                                               PYTATTLGDFMQQHVSKYGKIYRSNLFGEPTIVSADAGLNRFILQNEGRLFECSYPRSIG 117
                                 -QMVLQRRKFLQMKRRKYGFIYKTHLFGRPTVRVMGADNVRRILLGDDRLVSVHWPASVR 117
                                                                                                  LPALLASALCTFVLPLLLFLAAIKLWDLYCVSGRDRSCALPLPPGTMGFPFFGETL----
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416) 863-2653
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                                                                                                                                                                     85;
                                                                                                                                                                 Score 439; DB 4; Length 497; Pred. No. 3.7e-35; 5; Mismatches 226; Indels
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SEQ ID NO 405
LENGTH: 529
                                                                                                                                                                                                                                                                                Matches 117;
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Best Local Similarity
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Sequence 405, Appl
Patent No. 6410718
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 PRIOR APPLICATION NUMBER: US 08/975,316
PRIOR FILING DATE: 1997-11-21
PRIOR APPLICATION NUMBER: US 08/713,000
PRIOR FILING DATE: 1996-09-11
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              FILE REFERENCE: 11000.1003c4U
CURRENT APPLICATION NUMBER: US/09/615,192A
CURRENT FILING DATE: 2000-07-12
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   APPLICANT: Bloksberg, Leonard N.
APPLICANT: Havukkala, Ilkka
TITLE OF INVENTION: Materials and Methods
TITLE OF INVENTION: Modification of Plant
FILE REFERENCE: 11000.1003c4U
                                                                                                                                                                                                                                                                                                                                                                                                                                                                 PRIOR APPLICATION NUMBER: US PRIOR FILING DATE: 1998-10-09
                                                                                                                                                                                                                                                                                                                                                                                                                                                     NUMBER OF SEQ ID NOS:
                                                                                                                                                                                                                                                                                                                                                                                   TYPE: PRT
                                              176
163 VRDEVDIMVRIVAGSEGTAVNIGELVFELTRDIIYRAAFGTSSTEG-QDEFISILQEFSK 221
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                                                                                                   GGILGKWSMLVLVGDMHRDMRSIS-LNFLSHARLRTILLKDVERHTLFVLDSWQQNSIFS 175
                                                                                                                                     GLASLAKKYGGIFHLRMGFLHMVAVSSPDVARQVLQVHDGIFSNRPATIAISYLTYDRAD 130
                                                                                                                                                                    HVS----KYGKIYRSNLFGEPTIVSADAGLNRFILQNEGRLFE-------CSYPRSI 116
                                                                                                                                                                                                         PMTLLLSVVPLLLFLGLVARLRRKPPF--PPGPRGLPVIGNML
                                              AQDEAK - - - -
                                                                       -----MAFAHYGPFWRQMRKLCVMKLFSRKR-----
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21.9%;
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                                   -KFTFNLMAKHIMSMDPGEEETEQLKKEYVTFMK-----
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Pred. No. 1.7e-21;
4; Mismatches 204
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                                                                   ----- AESWE----S 162
                                                                                                                                                                                                                                                                                                         Length 529;
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APPLICANT: Chiang, Vincent L
APPLICANT: Carraway, Daniel T
APPLICANT: Smeltzer, Richard H
TITLE OF INVENTION: Production of Syringyl Lignin in
FILE REFERENCE: 50617
CURRENT APPLICATION NUMBER: US/08/991,677A
CURRENT FILING DATE: 1997-12-16
EARLIER APPLICATION UNMBER: US 60/033,381
EARLIER FILING DATE: 1996-12-16
NUMBER OF SEQ ID NOS: 11
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US-08-991-677-4
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SEQ ID NO 4
LENGTH: 511
TYPE: PRT
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LSLLFAGHETSSVAIALAIFFLQACPKAVEELREEHLEIARAKKELGESELNWDDYKKMD
                                                                                                                                                                                                                                                                                                            SIGGILGKWSMLVLVGDMHRDMRSIS-LNFLSHARLRTILLKDVERHTLFVLDSWQQNSI 173
                                          GSKNSEEVDTDMVDDLLAFYGEEAKVSESDD--
                                                                                                                                                       QL-----KKEYVTFMKGV---VSAPLNLPGTAYHKALQSRATILKFIERKMEERKLDIKE 255
                                                                                                                  QLFGAFNIADFIPWLKWVPQGINVRLN-------KARGALDGFIDKIIDDH---IQK
                                                                                                                                                                                             -SYRDEVDSAVRVVASNIGSTVNIGELVFALTKNITYRAAFGTISHEDQDEFVAILQEFS 210
                                                                                                                                                                                                                                                                         AD-----MAFAHYGPFWRQMRKLCVMKLFSRKR----
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                                                                                                                                                                                                                                                                                                                                                                                                                              HEALQPLPMTLFFIIPLLLLLGLVSR--LRQRLPYPPGPKGLPVIGNML-MMDQLTHRGL 62
                                                                                                                                                                                                                                                                                                                                                                                                                                                                   HHTLLPL-LLLPSLLSLLLFLILLKRRNRKTRFNLPPGKSGWPFLGETIGYLKPYTATTL 64
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     VVRFLHRKALKDVRYKGYDIPSGWKVLPVISAVHLDNSRYDQPNLFNPWRWQQQNNGASS
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                                                                          -DEAEMSKSDHVRKQRTDDDLLGWVLKHSNLSTEQILDLI 305
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                                      -- LQNSIKLTKDNIKAI
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; Sequence 6, Application US/08948564
; Patent No. 121512
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                                                                                                                                                                                                                                                                   Query Match
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APPLICANT:
                                                                                                                                                                                                                                                                                                                                                                                  SEQUENCE CHARACTERISTICS:
LENGTH: 513 amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                              TELECOMMUNICATION INFORMATION: TELEPHONE: 919-854-1400
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   CLASSIFICATION: 800
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
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MEDIUM TYPE: Floppy disk
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APPLICANT: Corbin, Frederick T.
APPLICANT: Corbin, Frederick T.
TITLE OF INVENTION: No. 6121512el Cytochrome P-450 Constructs and
TITLE OF INVENTION: Methods of Producing Herbicide-Resistant Trans
NUMBER OF SEQUENCES: 23
                                                                                                                                                                                                                                                                                                                             MOLECULE TYPE:
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 128
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                                   115 SIGGILGKWSMLVLVGDMHRDMRSISLNFLSHARLRTILLKDVERHTLFVL-----DSW 168
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                                                                                                                                                                                                                                               Match 10.4%; Score 279.5; Local Similarity 22.9%; Pred. No. 3.2
                                                                                                                                                                                                                                                                                                                                             TYPE: amino acid
TOPOLOGY: linear
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   REGISTRATION NUMBER: 37,092
REFERENCE/DOCKET NUMBER: 50
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CITY: Raleigh
STATE: No. 6121512th Carolina
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                APPLICATION NUMBER:
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                                                                                                                                                  LAFFISGLIF--FLKOKSKSKKFNLPPGPPGWPIVGNLFQVARSGKPFF----EYVNDV 67
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Bennett, Virginia C.
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 -RRNMVQNMLSSTRLKE--FRSVRDNAMDKLINRLKDEAE 173
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                                                                                                                                                                                                                              Mismatches 216;
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APPLICANT: LICHTEY, Jay
APPLICANT: Guido, Marco
FITTLE OF INVENTION: GENOTYPING OF HUMAN CYP3A4
FILE REFERENCE: SEQ-12P
CURRENT APPLICATION NUMBER: US/09/144,367
CURRENT FILING DATE: 1998-08-31
PRIOR APPLICATION NUMBER: 60/058,612
PRIOR APPLICATION NUMBER: 60/058,612
PRIOR FILING DATE: 1997-09-10
NUMBER OF SEQ ID NOS: 58
SOFTWARE: FASTSEQ for Windows Version 3.0
SEQ ID NO 2
SEQ ID NO 2
LENGTH: 503
TYPE: PRT
ORGANISM: H. Sapiens
US-09-144-367-2
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Best Local :
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RTDDDLLGWVLKHSNLSTEQILDLILSLLFAGHETSSVAIALAIFFLQACPKAVEELREE | | | ::|:||
                                                                                                                                                                                                 SAISIAEDEEWKRLRSLLSPTFTSGKLKEMVPIIAQYGDVLVRNLRREAETGKPVTL---
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                                                     FLIPILEVLNICVFPREVTNFL-RKSVKRMKESRLEDTQKHRV----DFLQL-MIDSQNSK
                                                                                                                                            DSWQQNSIFSA--QDEAKKFTFNLMAKHIMS-MDPGEEETEQLKK-EYV-TFMKGVVSAP : | | | | | ::| : :: | : | : | : |
                                                                                                                                                                                                                                                                       --FDMECHKKYGKVWGFYDGQQPVLAITDPDMIKTVLVKE--CYSVFTNRRPFGPVGFMK 115
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                                                                                       LNLPGTAYHKALQSRATILKFIERKMEERKLDIKEEDQEEEEVKTEDEAEMSKSDHVRKQ
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Pred. No. 1.4e-18;
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SEQ ID NO 18
LENGTH: 504
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TITLE OF INVENTION:
TITLE OF INVENTION:
TITLE OF INVENTION:
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CURRENT APPLICATION NUMBER: US/09/126,420A

CURRENT FILING DATE: 1998-07-30

PRIOR APPLICATION NUMBER: 60/054,351

PRIOR FILING DATE: 1997-07-31

NUMBER OF SEQ ID NOS: 27
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ORGANISM: Solanum melongena
                                                                                                                                                                                                                                                                                                         119
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                12 LLLLPSLLSLLLFLILLKRRNRKTRFNLPPGKSGWPFLGETIGY-LKPYTATTLGDFMQQ 70
                                                                                                                                                                         TAYHKALQSRATILKFIERKMEERKLDIKEEDQEEEEVKTEDEAEMSKSDHVRKQRTDDD
                                                                                                                                                                                                                                                                                                                                                                                 ---KYGPVLWLKEGSTYTMVVQTAQASEELFKNHDISFANRVIPDVNQAHSYYQGSLA--
                                                                                                                                                                                                                                                                                                                                                                                                                                                           IIILPA-----FILFFSQKNTTKSSYRPPGPPGLPIFGNMFELGTEPYKKMAV----LRQ
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EPNRKFEDS---
                                   RAKKELGESELNWDDYKKMDFTQCVINETLRLGNVVRFL-HRKALKDVRYKGYDIPSGWK 404
                                                                         -----EPAKLSEHEIKIFVLEMFLAGTETTSSSVEWALTELLRHPEAMAKVKTEISQAI
                                                                                                             LLGWVLKHSNLSTEQILDLILSLLFAGHETSSVAIALAIFFLQACPKAVEELREEHLEIA
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                                                                                                                                                 LKKFDLQSLRKKMARDMGKAVEIMSMFLKE--REEERKKGTEKGKDFLDVLLEFQGTGKD
                                                                                                                                                                                                                                                                 ----EAKKE-----GVVSAPLNLPG
                                                                                                                                                                                                                                                                                                       -----TAPYGPFWRFQRRICTIEMFVHKKISE--TEPVRRKCVDNMLKWIEKEANSAEK
                                                                                                                                                                                                                                                                                                                                         LGKWSMLVLVGDMHRDMRSI-SLNFLSHARLRTILLKDVERHTLFVLDSWQQNSIFSAQD 178
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     - IDAVLPNK----APPTYDTVLQMEYLDMVVNETLRLFPIAMRLERVCKKDVEINGMFIP
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WERCK-REICHART, DANIELE
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TÜBEROSUS AND ITS APPLICATIONS AS BICCATALIST IN
PARTICULAR FOR THE DEGRADATION OF ENVIRONMENTAL
POLLUTANTS AND FOR ALTERING THE RESISTANCE OF PLANTS S
DIENLPYMQAVLKESLRLHPPLPFLIPRETIQDTKFMGYDVPKDTQ
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        10.1%; Score 271; DB 4; 21.7%; Pred. No. 2.2e-18;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Length 504;
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APPLICANT: WOON, KYUNG KO
APPLICANT: YOUNG, SOON KIM
TITLE OF INVENTION: A CYTOCHROME P450 GENE HIGHLY EXPRESSED IN TITLE OF INVENTION: INCOMPATIBLE INTERACTION
FILE REFERENCE: 10324/P64443USO
CURRENT APPLICATION NUMBER: US/09/499,302A
CURRENT FILING DATE: 2000-02-07
NUMBER OF SEQ ID NOS: 10
SOFTWARE: PATENTIN Ver. 2.1
SEQ ID NO 2
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Best Local
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Matches 114;
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ORGANISM: Capsicum
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Local Similarity
                                                                                                   GYDIPSGWKVLPVISAVHLDNSRYDQPNLFNPWRWQQQNNGASSSGSGSESTWGNNYMPF 455
                                                                                                                                                                                                                                                                                                                                                                      NLTDKIFWFTSSVTCRSALGKICRDQD-----KLIIFMREIISLTGGFSIADFFPTWKM 224
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ---GKWSMLVLVGDMHRDMRSISLNFLSHARLRTILLKDVERHTLFVLDS----WQQNSIF 174
                                    GGGPRLCAGSELAKLEMAVFIHHLVLKFNWELAEDDQPFAFPFVDFPNGLP
                                                                                                                                                                      LREEHLEIARAKKELGESELNWDDYKKMDFTQCVINETLRLGNVVRFL-HRKALKDVRYK 395
                                                                                                                                                                                                                                                                                                                                                                                                                                            SPYGEWT-----RQIRKICILELLSAKM-VKFFSSIRQDELSMMVSSIRTMPNFPV 170
 GAGRRICPG----
                                                                      GYNIPFKTRVIVNAWAIGRDPESWDDPESFSPERF--ENSSVDFLGS-----HHQFIPF
                                                                                                                                                                                                                        VQISITDDN----
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                                                                                                                                             AQAEVRQVLKEKK--GFQQIDLDELK---YLKLVIKETLRMHPPIPLLVPRECMKDTKID
                                                                                                                                                                                                                                                                                                                                 LNLPGTAYHKALQSRATILKFIERKMEERKLDIKEEDQEEEEVKTEDEAE----MSKSDH 276
                                                                                                                                                                                                                                                                                                                                                                                                          SAODEAKKFTFNLMAKHIMSMDPGEEETEQLKKEYVTFMKGVVSAP-------
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                                                                                                                                                                                                                      -IKSILVDMFSAGSETSSTTIWALAEMMKKPSVLAK 329
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Score 268.5; DB 4
Pred. No. 3.9e-18;
0; Mismatches 208
-MKFG--LANVGQPLAQLLYHFDRKLP
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469
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RESULT 14

RESULT 15 US-09-126-420A-26

Sequence 26, Application US/09126420A Patent No. 6376753
GENERAL INFORMATION:

APPLICANT:

BATARD,

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APPLICANT: BATARD, YANNICK
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Matches 113;
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CURRENT APPLICATION UMMBER: US/09/126,420A

CURRENT FILING DATE: 1998-07-30

PRIOR APPLICATION NUMBER: 60/054,351

PRIOR FILING DATE: 1997-07-31
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TYPE: PRT
ORGANISM: Solanum melongena
    435
                                            487
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                                                                                                                                                                                                                                                                                                                                                                                                                                 176
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              105
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                                                                                                                                                                                                                                                                                                                                                                                       258
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      162 LFVLDSWQQNSIFSAQD--EAKKF----TFNLMAKHIMSMDPGEEETEQLKKEYVTFMKG 215
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LPHNVSP
                                         LAEDDQP
                                                                                                                           RWQQQNNGASSSGSGSFSTWGNNY--MPFGGGPRLCAGSELAKLEMAVFIHHLVLKFNWE 486
                                                                                                                                                                                                                                                                                                                                                                                                                                                     VVSAPLNLPGTA-----YHKALQ-----SRATILKFIERKMEERKLDIKEED :: | | :: | | | | :: | | | |
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          GRLFECSYPRSIGGILGKWSM-LVLVGDMHRDMRSI-SLNFLSHARL-RTILLKDVERHT 161
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    WLKIGSSMNTMVIQTANSASELFRNHDVS-----FSDRPIVDVNLAHNYY-----
                                                                                                                                                                                                                                                       LAGTETTSSSVEWALTELLRHPQAMAKVKLETLQVIGPNKKFEECDID-----SLPYVQA 324
                                                                                                                                                                                                                                                                                                                                                                                  QEEEEVKTEDEAEMSKSDHVRKQRTDDDLLGWVL-----KHSNLSTEQILDLILSLL
                                                                                 RFLE-----
                                                                                                                                                                   VLKEQLRLHPPLPLLIPRKAIQDTKFMGYDIPKGTQVLVNAWAIGRDPEYWDNPFEFKPE
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    441
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     1997-07-31
os: 27
                                                                                   SKVDVKGQNYELIPFGAGRRMCVGLPLGHRMMHFTFGSLLHEFDWE
                                                                                                                                                                                                                                                                                                                                             -----KNRSIKDLLDVLIDFEGSGKDEPDKLSEDEIIVIILEMF 269
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     10.0%; Score 268; DB 4; 23.2%; Pred. No. 3.9e-18 tive 80; Mismatches 18
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; SEQ ID NO 26
; LENGTH: 494
; TYPE: PRT
; ORGANISM: Rattus norvegicus
US-09-126-420A-26
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             TITLE OF INVENTION: PURIFIED CYTOCHORME P450 CYP76B1 FROM HELIANTHUS TITLE OF INVENTION: TUBEROSUS AND ITS APPLICATIONS AS BIOCATALYST IN TITLE OF INVENTION: PARTICULAR FOR THE DEGRADATION OF ENVIRONMENTAL TITLE OF INVENTION: POLLUTANTS AND FOR ALTERING THE RESISTANCE OF PLANTS S FILE REFERENCE: 03715.0032

CURRENT APPLICATION NUMBER: US/09/126,420A

CURRENT FILING DATE: 1998-07-30

PRIOR APPLICATION NUMBER: 60/054,351

PRIOR FILING DATE: 1997-07-31

NUMBER OF SEQ ID NOS: 27
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    173 YLSRTVSNVISSIVFGDREDYEDKEFLSLLRMMLGSFQFTATSTGQLYEMFSSVMK----
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      72 VSKYGKIYRSNLFGEPTIV--SADAGLNRFILQNE---GRLFECSYPRSIGGILGKWSML 126
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AFVPFSIGKRYCFGEGLARMELFLFLINIMQNFCFKSPQAPQDIDVSPRLVGFATIP 484
                                                                                                                                                                          DVRYKGYDIPSGWKVLPVISAVHLDNSRYDQPNLFNPWRWQQQNNGASSSGSGSESTWGN 450 | ::: :: | | :: | | :: | | : | | : | | : | | : | | : | | : | | : | | | : | | | : | | | : | | | : | | | | : | | | | : | | | | | : | | | | : | | | | : | | | | : | | | | : | | | | | : | | | | | : | | | | | : | | | | | : | | | | | : | | | | : | | | | : | | | | : | | | : | | | : | | | : | | | : | | : | | : | | : | | : | | : | | : | : | | : | : | | : | : | | : | : | : | | : | : | : | | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | 
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Search completed: March 30, 2003, 12:08:19 Job time: 40 secs

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Minimum DB seq length: 0
Maximum DB seq length: 2000000000
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Perfect score:
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Listing first 45 summaries
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2681
1 MFETEHHTLLPLILLPSLLS......FAFPFVDFPNGLPIRVSRIL 513
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: /cgn2_6/ptodata/1/pubpaa/US08_NEW_PUB.pep: *
: /cgn2_6/ptodata/1/pubpaa/PCT_NEW_PUB.pep: *
: /cgn2_6/ptodata/1/pubpaa/US06_NEW_PUB.pep: *
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

## SUMMARIES

1 2 3 3 4 4 4 4 7 7 7 1 1 1 1 1 1 1 1 1 1 1 1 1	Result No.
290.5 290.5 285.89 285.89 285.5 207.5 257.5 257.5 257.7 257.7 244.2 244.2 244.2 244.2 244.2 244.2 244.3 244.3 244.3 244.3 244.3 244.3 244.3 244.3 244.3 244.3 244.3 244.3 244.3 244.3 244.3 244.3 244.3 244.3 244.3 244.3 244.3 244.3 244.3 244.3 244.3 244.3 244.3 244.3 244.3 244.3 244.3 244.3 244.3 244.3 244.3 244.3 244.3 244.3 244.3 244.3 244.3 244.3 244.3 244.3 244.3 244.3 244.3 244.3 244.3 244.3 244.3 244.3 244.3 244.3 244.3 244.3 244.3 244.3 244.3 244.3 244.3 244.3 244.3 244.3 244.3 244.3 244.3 244.3 244.3 244.3 244.3 244.3 244.3 244.3 244.3 244.3 244.3 244.3 244.3 244.3 244.3 244.3 244.3 244.3 244.3 244.3 244.3 244.3 245.3 246.3 246.3 246.3 246.3 246.3 246.3 246.3 246.3 246.3 246.3 246.3 246.3 246.3 246.3 246.3 246.3 246.3 246.3 246.3 246.3 246.3 246.3 246.3 246.3 246.3 246.3 246.3 246.3 246.3 246.3 246.3 246.3 246.3 246.3 246.3 246.3 246.3 246.3 246.3 246.3 246.3 246.3 246.3 246.3 246.3 246.3 246.3 246.3 246.3 246.3 246.3 246.3 246.3 246.3 246.3 246.3 246.3 246.3 246.3 246.3 246.3 246.3 246.3 246.3 246.3 246.3 246.3 246.3 246.3 246.3 246.3 246.3 246.3 246.3 246.3 246.3 246.3 246.3 246.3 246.3 246.3 246.3 246.3 246.3 246.3 246.3 246.3 246.3 246.3 246.3 246.3 246.3 246.3 246.3 246.3 246.3 246.3 246.3 246.3 246.3 246.3 246.3 246.3 246.3 246.3 246.3 246.3 246.3 246.3 246.3 246.3 246.3 246.3 246.3 246.3 246.3 246.3 246.3 246.3 246.3 246.3 246.3 246.3 246.3 246.3 246.3 246.3 246.3 246.3 246.3 246.3 246.3 246.3 246.3 246.3 246.3 246.3 246.3 246.3 246.3 246.3 246.3 246.3 246.3 246.3 246.3 246.3 246.3 246.3 246.3 246.3 246.3 246.3 246.3 246.3 246.3 246.3 246.3 246.3 246.3 246.3 246.3 246.3 246.3 246.3 246.3 246.3 246.3 246.3 246.3 246.3 246.3 246.3 246.3 246.3 246.3 246.3 246.3 246.3 246.3 246.3 246.3 246.3 246.3 246.3 246.3 246.3 246.3 246.3 246.3 246.3 246.3 246.3 246.3 246.3 246.3 246.3 246.3 246.3 246.3 246.3 246.3 246.3 246.3 246.3 246.3 246.3 246.3 246.3 246.3 246.3 246.3 246.3 246.3 246.3 246.3 246.3 246.3 246.3 246.3 246.3 246.3 246.3 246.3 246.3 246.3 246.3 246.3 246.3 246.3 246.3 246.3 246.3 246.3 246.3 246.	Score
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sequence 3, Appli Sequence 4, Appli Sequence 4, Appli Sequence 69, Appli Sequence 69, Appl Sequence 10, Appl Sequence 12, Appl Sequence 2, Appli Sequence 19, Appli Sequence 19, Appli Sequence 19, Appli Sequence 18, Appli Sequence 18, Appli Sequence 18, Appli Sequence 18, Appli Sequence 3, Appli Sequence 3, Appli Sequence 3, Appli Sequence 3, Appli Sequence 3, Appli Sequence 3, Appli	

45	44	43	42	41	40	39	38	37	36	35	34	33	32	31	30	29	28	27	26	25	24	23	22	21
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US-09-989-730-264	US-09-990-444-264	US-09-989-735-264	US-10-063-547-54	US-09-989-293A-264	US-09-992-598-264	US-09-925-299-905	US-09-925-299-905	US-10-141-755-108	σs-10-121-050-108	US-10-142-423-108	US-10-123-262-108	US-10-142-419-108	US-10-140-002-108	US-10-143-114-108	US-10-142-431-108	US-10-140-474-108	-0	US-10-176-921-108	US-10-176-918-108	US-10-175-746-108	JS-10-140-470-108	US-10-123-904-108	US-10-121-049-108	US-10-028-072-108
Sequence 264,	Sequence 264,	Sequence 264,		264,	Sequence 264,	Sequence 905,	Sequence 905,		•	108,	•	•	•	•	•	•	•	-	Sequence 108,	108,	•	•	•	Sequence 108,
App	App	App	Appl	App	App	, App	App	App	App	App	App	App	App	App	App	App	App	App	App	App	App	App	App	App

## ALIGNMENTS

04 A0	Db Qy	US-
Qy 72 VSKYGKIYRSNLFGEPTIVSADAGLNRFILQNEGRLFECSYPRSIGGILGKWSM 125	Query Match  10.9%; Score 292; DB 9; Length 516; Best Local Similarity 23.6%; Pred. No. 7.8e-16; Matches 120; Conservative 92; Mismatches 220; Indels 76; Gaps 17;  Matches 120; Conservative 92; Mismatches 220; Indels 76; Gaps 17;  Qy 12 LLLLPSLLSLLLFLILLKRRNRKTRFNLPPGKSGWPFLGETIGYLKPYTATTLGDFMQQH 71  :::  ::   :	US-10-067-534-3 US-10-067-534-3 US-10-067-534-3  Esquence 3, Application US/10067534  Publication No. US20020187538A1  GENERAL INFORMATION: APPLICANT: Essenberg, Margaret K. APPLICANT: Chen, Xiao-Ya  APPLICANT: Luo, Ping APPLICANT: Wang, Yan-Hong APPLICANTION: USABER: US/10/067,534  CURRENT APPLICATION NUMBER: US/07/067,534  CURRENT FILING DATE: 2002-02-07  PRIOR APPLICATION NUMBER: US 60/267,160  PRIOR FILING DATE: 2001-02-07  INUMBER OF SQO ID NOS: 19  SGO ID NO 3  LENGTH: 516  TYPE: PRT  ORGANISM: Arabidopsis thaliana  US-10-067-534-3
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SEQ ID NO 4
LENGTH: 514
TYPE: PRT
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APPLICANT: Chiang, Vincent Lee C.
APPLICANT: Li, Laigeng
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Best Local
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Patent No. US20020124281A1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 NUMBER OF SEQ ID NOS: 14
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    FILE REFERENCE: 066040-9718
CURRENT APPLICATION NUMBER: US/09/947,027
CURRENT FILING DATE: 2001-09-05
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    APPLICANT: L1, Laigeng
TITLE OF INVENTION: METHODS FOR SIMULTANEOUS CONTROL OF LIGHTN CONTENT AND COMPOSITIC
TITLE OF INVENTION: CELLULOSE CONTENT IN PLANTS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        PRIOR APPLICATION NUMBER: PRIOR FILING DATE: 2000-09
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KAVEELREEHLEIARAKKELGESELNWDDYKKMDFTQCVINETLRLGNVVRFLHRKALKD
                                                                                                                            NLPGTAYHKALQSRATILKFIERKMEERKLD--IKEEDQEEEEVKTEDEAEMSKSD----
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                                                                                             FIPWLGWIDPQGLSARLVK--ARKALDRFIDSIIDDHIQKRKQNKFSEDAETDMVDDMLA
                                                                                                                                                                                         LFVLDSWQQNSIFSAQDEAKKFTFNLMAKHIMSMDPGEEETEQLKKEYVTFMKGVVSAPL 221
                                                                                                                                                                                                                        ---MAFAHYGPFWRQMRKLCVMKLFSRKRAESWESVRDEVDSMLKTVEANIGKPVNLGEL 177
                                                                                                                                                                                                                                                                                                                  HVSKYGKIYRSNLFGEPTIVSADAGLNRFILQNEGRLFE------CSYPRSIGGIL
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                                FYGEEARKVDESDDL----QKAISLTKDNIKAIIMDVMFGGTETVASAIEWVMAELMKSP
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                                                              ----HVRKQRTDDDLLGWVLKHSNLSTEQILDLILSLLFAGHETSSVAIALAIFFLQACP 331
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SOFTWARE: PatentIn version 3.0
SEQ ID NO 4
LENCTH: 514
TYPE: PRT
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TITLE OF INVENTION: METHODS FOR SIMULTANEOUS CONTROL OF LIGHIN CONTENT ,
TITLE OF INVENTION: COMPOSITION, AND
TITLE OF INVENTION: COMPOSITION, AND
TITLE OF INVENTION: COMPOSITION, IN PLANTS
FILE REFERENCE: 066040-9718
CURRENT FILING DATE: 2002-03-06
PRIOR ADDITORMATE: 2002-03-06
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Best Local Similarity
Matches 123; Conserv
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PRIOR APPLICATION NUMBER: 09/947,027
PRIOR FILING DATE: 2001-09-05
PRIOR APPLICATION NUMBER: 60/230,086
PRIOR RILING DATE: 2000-09-05
NUMBER OF SEQ ID NOS: 14
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332 KAVEELREEHLEIARAKKELGESELNWDDYKKMDFTQCVINETLRLGNVVRFLHRKALKD
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                                                                                                             ----HVRKQRTDDDLLGWVLKHSNLSTEQILDLILSLLFAGHETSSVAIALAIFFLQACP 331
                                                                                                                                                                        FIPWLGWIDPQGLSARLVK--ARKALDRFIDSIIDDHIQKRKQNKFSEDAETDMVDDMLA
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                                                           FYGEEARKVDESDDL----QKAISLTKDNIKAIIMDVMFGGTETVASAIEWVMAELMKSP
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US-09-796-256A-4

GENERAL

APPLICANT: Chiang, Vincent L

INFORMATION:

Sequence 4, Application US/09796256A Patent No. US20020078477A1

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359 YLKCVLKEVLRLHPPIPLLLHETAEDAEVGGYYIPAKSRVMINACAIGRDKNSWADPDTF
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           APPLICANT: Carraway, Daniel T
APPLICANT: Smeltzer, Richard H
TITLE OF INVENTION: Production of Syringyl Lignin in Gymnosperms
                                                                                                                                                        306 LSLLFAGHETSSVAIALAIFFLQACPKAVEELREEHLEIARAKKELGESELNWDDYKKMD 365
                                                                                                                                                                                          258 GSKNSEEVDTDMVDDLLAFYGEEAKYSESDD-----LQNSIKLTKDNIKAI
                                                                                                                                                                                                                                                    211 QLFGAFNIADFIPWLKWVPQGINVRLN------KARGALDGFIDKIIDDH---IQK 257
                                                                                                                                                                                                                                                                                                                      152 - SVRDEVDSAVRVVASNIGSTVNIGELVFALTKNITYRAAFGTISHEDODEFVAILQEFS
                                                                                                                                                                                                                                                                                                                                                    174 FSAQDE-----EETE 203
                                                                                                                                                                                                                                                                                                                                                                                                                    115 SIGGILGKWSMLVLVGDMHRDMRSIS-LNFLSHARLRTILLKDVERHTLFVLDSWQQNSI 173
                                                                                                                                                                                                                                                                                                                                                                                                                                                  63 AKLAKO----YGGLEHLKMGFLHMVAVSTPDMARQVLQVQDNIFSNRPATIAISYLTYDR 118
                                                                                     FTQCVINETLRLGNVVRFLHRKALKDVRYKGYDIPSGWKVLPVISAVHLDNSRYDQPNLF 425
                                                                                                                          MDVMFGGTETVASAIEWÄMTELMKSPEDLKKVQQELAVVVGLDRRVEEK-----DFEKLT 358
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                6 HHTLLPL-LLLPSLLSLLLFLILLKRRNRKTRFNLPPGKSGWPFLGETIGYLKPYTATTL 64
                                                                                                                                                                                                                      EDQEESEVKTE-----DEAEMSKSDHVRKQRTDDDLLGWVLKHSNLSTEQILDLI 305
                                                                                                                                                                                                                                                                                      QL-----KKEYVTFMKGV---VSAPLNLPGTAYHKALQSRATILKFIERKMEERKLDIKE 255
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       440 FEFIPEGSGRRSCPGMQLGLYTLDLAVAHLLHCFTWELPDGMKPSELDMTDMFGLTAPRA 499
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                                                                                                                                                                                                                                                                                                                                                                                    AD-----MAFAHYGPFWROMRKLCVMKLFSRKR------AESWE---- 151
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  GDFMQOHVSKYGKIYRSNLFGEPTIVSADAGLNRFILQNEGRLFE------CSYPR 114
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   HEALQPLPMTLFFIIPLLLLLGLVSR--LRQRLPYPPGPKGLPVIGNML-MMDQLTHRGL 62
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Length 511;
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: OTHER INFORMATION: Xaa equals stop translation
US-09-739-254-69
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Best Local Similarity 23.4
124; Conservative
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SEQ ID NO 69
LENGTH: 502
TYPE: PRT
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389 LKDVRYKGYDIPSGWKVLPVISAVHLDNSRYDQDNLFNPWRWQQQNNGASSSGSGSESTW 448
                                                   329 YPNIQGQVQKE-IDLIMGP----NGKPSWDDKCKMPYTEAVLHEVLRFCNIVPLGIFHAT
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EARLIER FILING DATE: 2000-02-23
EARLIER APPLICATION NUMBER: PCT/US99/19330
EARLIER FILING DATE: 1999-08-24
EARLIER APPLICATION NUMBER: 60/097,917
PARTITUD TATES. 1008-02-26
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GENERAL INFORMATION:
                                                                          285 DQGKND-------PSSTFSKENLIFSVGELIIAGTETTINVLRWAILFMAL 328
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EARLIER APPLICATION NUMBER: 60/
EARLIER FILING DATE: 1998-08-31
                                                                                                                                             270 EMSKSDHVRKQRTDDDLLGWVLKHSNLSTEQILDLILSLLFAGHETSSVAIALAIFFLQA 329
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      NUMBER OF SEQ ID NOS: 170
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                                                                                                                                                                             225 SVFLYNAFPWIGILPFGKHQQLFRNAAVVYDFLSRLIEKASVNRKPQLPQHFVDAYLDEM 284
                                                                                                                                                                                                                                             217
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ORGANISM: Homo sapiens FEATURE:
                                                                                                                                                                                                                                                                           174 FSAQDEAKK----FTFNLMAKHIMS-----MDPGE----EETE-----QLKKEYVTFNKGV 216
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          APPLICANT: Rosen et al.
TITLE OF INVENTION: 49 Human Secreted Proteins
FILE REFERENCE: PZ032P1
                                                                                                                                                                                                                                                                                                           124 LLNSRYGRGWV------DHRRLAVNSFRYFGYGQ-----KSFESKIL-----EETKF 164
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                                                                                                                                                                                                                                                                                                                                                                                                         67 FMQQHVSKYGKIYRSNLFGEPTIVSADAGLNRFILQNEGRLFECSYP-----RSIGG
                                                                                                                                                                                                                                                                                                                                                                                                                                           14 LGGALFILLFALGVRQLLKQRR----PMGFPPGPPGLPFIGNI-----YSLAASSELPHV
                                                                                                                                                                                                                                                                                                                                                                                                                                                                         15 LPSTLSLILFLI----LIKRRNRKTRFNLPPGKSGWPFLGETIGYLKPYTATTLGD----
                                                                                                                                                                                                             VSAPLN-----LPGTAYHKALOSRATILKFIERKMEERKLDIKEEDQEEEEVKTEDEA 269
                                                                                                                                                                                                                                             FNDAIETYKGRPFDFKQLITNAVSNITNLIIFGERFTYEDTDFQHMIELFSENVELAASA 224
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                                                                                                                                                                                                                                                                                                                                           ILGK-----WSMLVLVGDMHRDMRSISLNFLSHARLRTILLKDVERHTLFVLDSWQQNSI 173
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              10.6%; Score 285.5; DB 10; 23.4%; Pred. No. 2.6e-15; ac. Mismatches 210;
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                                                                                   388
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22;

LENGTH: 511 TYPE: PRT ORGANISM: Liquidambar styraciflua US-09-796-256A-4

NUMBER OF SEQ ID NOS: 11
SOFTWARE: Patentin Ver. 2.1
LPMC.

PRIOR FILING DATE:

PRIOR APPLICATION NUMBER: US60/033381 PRIOR FILING DATE: 1996-12-16

APPLICATION NUMBER: 08/991677

Query Match Best Local Similarity

Matches

121;

Conservative

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US-09-904-615-69
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Best Local :
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LENGTH: 502
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APPLICANT: ROSEN et al.
APPLICANT: ROSEN et al.
TITLE OF INVENTION: 49 Human Secreted
FILE REFERENCE: PZ032P1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Sequence 69, Application US/09904615 Patent No. US20020026040A1
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PRIOR FILING DATE: 2000-02-23
PRIOR APPLICATION NUMBER: 60/097,917
PRIOR FILING DATE: 1998-08-25
PRIOR APPLICATION NUMBER: 60/098,634
PRIOR APPLICATION NUMBER: 60/098,634
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CURRENT FILING DATE: 2001-07-16
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NUMBER OF SEQ ID NOS: 170
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LOCATION: (502)
OTHER INFORMATION: Xaa equals stop translation
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Local Similarity 23.4%;
GNNYMPFGGGPRLCAGSELAKLEMAVFIHHLV----LKFNWELAEDDQP 493
                                                        SEDAVVRGYSIPKGTTVITNLYSVHFDEKYWRDPEVFHPERF-----LDSSGYFAK-
                                                                                             LKDVRYKGYDIPSGWKVLPVISAVHLDNSRYDQPNLFNPWRWQQQNNGASSSGSGSFSTW
                                                                                                                                                     CPKAVEELREEHLEIARAKKELGESELNWDDYKKMDFTQCVINETLRLGNVVRF-LHRKA
                                                                                                                                                                                                                                 EMSKSDHVRKQRTDDDLLGWVLKHSNLSTEQILDLILSLLFAGHETSSVAIALAIFFLQA
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                                                                                                                                YPNIQGQVQKE-IDLIMGP----NGKPSWDDKCKMPYTEAVLHEVLRFCNIVPLGIFHAT
                                                                                                                                                                                                                                                                                                                     VSAPLN-----LPGTAYHKALQSRATILKFIERKMEERKLDIKEEDQEEEEVKTEDEA
                                                                                                                                                                                                                                                                                                                                                            FNDAIETYKGRPFDFKQLITNAVSNITNLIIFGERFTYEDTDFQHMIELFSENVELAASA 224
                                                                                                                                                                                                                                                                                                                                                                                             FSAQDEAKK----FTFNLMAKHIMS-----MDPGE----EETE-----QLKKEYVTFMKGV
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US-10-067-668-10
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APPLICANT: Glucksmann, Maria Alexandra
TITLE OF INVENTION: 33312, 33303, 32579, NOVEL HUMAN
TITLE OF INVENTION: CYTOCHROME P450 FAMILY MEMBERS AND USES THEREOF
FILE REFERENCE: 10448-136001
CURRENT APPLICATION NUMBER: US/10/067,668
CURRENT FILING DATE: 2002-02-04
PRIOR APPLICATION NUMBER: 60/266,140
PRIOR APPLICATION NUMBER: 50/266,140
PRIOR FILING DATE: 2001-02-02
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SOFTWARE: FastSEQ for Windows Version 4.0
SEQ ID NO 10
LENGTH: 496
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Matches 126;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Query Match
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 436
                                     460
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Local Similarity
RNCLGERLARMELFLFLATLLQRF-----PELELAVPPGDIPSLTPKPELGLP
                                                                                                                                                                       LEIARAKKELGESELNWDDYKKMDFTQCVINETLRLGNVV-RFLHRKALKDVRY-KGYDI 399
                                                                                                                                                                                                                                            TDDDLLGWVLKHSNLSTEQILDLILSLLFAGHETSSVAIALAIFFLQACPKAVEELREEH
                                 RLCAGSELAKLEMAVFIHHLVLKFNWELAEDDQPFAFPFVDFPN-----GLP 506
                                                                                                         PSGWKVLPVISAVHLDNSRYDQPNLFNPWRWQQQNNGASSSGSGSFSTWGNNYMPFGGGP 459
                                                                                                                                                                                                                          KAAKDLKDYLDKLIEERRETLEPAGDPRRLDIGFLDSLLLEAKREGGNPKSE------
                                                                                                                                                                                                                                                                                                                                   QSRATILKFIERKMEE-------RKLDIKEEDQEEEEVKTEDEAEMSKSDHVRKQR
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           PEAVKEVLIDKGEEFAKGRGDENPTEPWLSKGYREQGLLFSDNGPKWRKLRRFSLLTLRF 115
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              AGLNRFILQNEGRL-----FECSYPRSIGGILGKWSMLVLVGDMHRDMRSISLNFL-- 144
                                                                        PKGTLVIVNLYSLHRDPKVFPNPEEFDPERFLDENGKFKKSYA-----FLPFGAGP
                                                                                                                                                DEVIGRDR----SPTYDVDARAQMPYLDAVIKETLRLYPVVPLLLPRVATKDTEIPDGYLI
                                                                                                                                                                                                                                                                                                                                                                                                              -----SHARLRTILLKDVERHTLFVLDSWQQNS-IFSAQDEAKKFTFNLMAKHIMS
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Pred. No. 1.8e-14;
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US-09-945-301-4

Sequence 4, Application US/09945301 Patent No. US20020090699A1 GENERAL INFORMATION:
APPLICANT: Millennium Pharmaceutic

Pharmaceuticals,

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RESULT 9
US-10-067-668-12
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APPLICANT: Tsai, Fong Ying
TITLE OF INVENTION: 27439, NOVEL HUMAN HYDRO
TITLE OF INVENTION: THEREFOR
FILE REFERENCE: 38155-20036.00
CURRENT APPLICATION NUMBER: US/09/945,301
CURRENT FILING DATE: 2001-08-31
PRIOR APPLICATION NUMBER: US 60/229,301
PRIOR FILING DATE: 2000-09-01
                                                                                                                                             Sequence 12, Application US/10067668 Publication No. US20030022334A1 GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              SOFTWARE: FastSEQ for Windows Version 4.0
SEQ ID NO 4
LENGTH: 496
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                                                                    APPLICANT: Glucksmann, Maria Alexandra
TITLE OF INVENTION: 33312, 33303, 32579, NOVEL HUMAN
TITLE OF INVENTION: CYTOCHROME P450 FAMILY MEMBERS
FILE REFERENCE: 10448-136001
CURRENT APPLICATION NUMBER: US/10/067,668
CURRENT FILING DATE: 2002-02-04
PRIOR APPLICATION NUMBER: 60/266,140
PRIOR FILING DATE: 2001-02-02
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 TYPE: PRT
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         -----SHARLRTILLKDVERHTLFVLDSWQQNS-IFSAQDEAKKFTFNLMAKHIMS 194
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  AGLNRFILQNEGRL-----FECSYPRSIGGILGKWSMLVLVGDMHRDMRSISLNFL-- 144
                                                                                                                                                                                                                                                                      RNCLGERLARMELELFLATILORF-----PELELAVPPGDIPSLTPKPELGLP 483
                                                                                                                                                                                                                                                                                                              RLCAGSELAKLEMAVFIHHLVLKFNWELAEDDQPFAFPFVDFPN-----GLP 506
                                                                                                                                                                                                                                                                                                                                                                                                                         DEVIGEDR----SPTYDVDARAQMPYLDAVIKETLELYPVVPLLLPRVATKDTEIPDGYLI
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                                                                                                                                                                                                                                                                                                                                                 PKGTLVIVNLYSLHRDPKVFPNPEEFDPERFLDENGKFKKSYA-----FLPFGAGP
                                                                                                                                                                                                                                                                                                                                                                                   PSGWKVLPVISAVHLDNSRYDQPNLFNPWRWQQQNNGASSSGSGSFSTWGNNYMPFGGGP 459
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Pred. No. ]
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                                                                                                             NOVEL HUMAN
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US-09-992-901-2
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                                                                                                                     ; ORGANISM: Arabidopsis thaliana US-09-992-901-2
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SOFTWARE: FastSEQ for
SEQ ID NO 12
                                                                                                                                                                   SOFTWARE: FastSEQ
SEQ ID NO 2
LENGTH: 520
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                                                    Matches
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                                                                                  Query Match
                                                                                                                                                                                                                                                                   PRIOR APPLICATION NUMBER: US 09/527,073
PRIOR FILING DATE: 2000-03-16
PRIOR APPLICATION NUMBER: US 60/124570
PRIOR FILING DATE: 1999-03-16
PRIOR APPLICATION NUMBER: US 60/170,931
PRIOR FILING DATE: 1999-12-14
                                                                                                                                                                                                                                                                                                                                                                                                     APPLICANT: Chory, Joanne
TITLE OF INVENTION: GENETICALLY MODIFIED PLANTS HAVING
TITLE OF INVENTION: MODULATED BRASSINOSTEROID SIGNALING
FILE REFERENCE: SALKINS.024DV1
                                                                                                                                                                                                                                    PRIOR APPLICATION NUMBER: US 60/172,832 PRIOR FILING DATE: 1999-12-20
                                                                                                                                                                                                                                                                                                                                                                      CURRENT APPLICATION NUMBER: US/09/992,901
CURRENT FILING DATE: 2001-11-14
                                                                                                                                                                                                                                                                                                                                                                                                                                                          APPLICANT: Neff, Michael M. APPLICANT: Chory, Joanne
                                                                                                                                                                                                                    NUMBER OF SEQ ID NOS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           TYPE: PRT
ORGANISM: Artificial Sequence
                                                                                                                                                       TYPE: PRT
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                                                 / Match 9.6%;
Local Similarity 23.8%;
nes 136; Conservative 9
1 MFETEHHTLLPLLLLPSLLSLLLFLILLKR-----RNRKTRFNL-PPGKSGWP---FLG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  -GLP 506
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                                                 Score 256.5; DB 10;
Pred. No. 6.3e-13;
5; Mismatches 225;
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Pred. No. 3e-14;
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                                                                                  DB 10;
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US-09-796-138-19
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US-09-796-138-19
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                                                                                                                                     Best Local Similarity Matches 120; Conserv
                                                                                                                                                                                  Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                TITLE OF INVENTION: Mycobacterium tuberculosis CYP51 HIGH RESOLUTION STUCTURE, TITLE OF INVENTION: AND TITLE OF INVENTION: NUCLEIC ACIDS, AND THERAPEUTIC AND SCREENING METHODS TITLE OF INVENTION: RELATING TO SAME FILE REFERENCE: Attorney Docket No. US20020031782A1 1242-17-2 CURRENT APPLICATION NUMBER: US/09/796,138 CURRENT FILING DATE: 2001-02-28 CURRENT FILING DATE: 2001-02-28
                                                                                                                                                                                                                                                                                                                                                                   PRIOR APPLICATION NUMBER: 09/345,218 PRIOR FILING DATE: 1999-06-30 NUMBER OF SEQ ID NOS: 21
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                APPLICANT: Waterman, Michael R. APPLICANT: Bellamine, Aouatef APPLICANT: Podust, Larissa M.
                                                                                                                                                                                                                                              TYPE: PRT ORGANISM: Penicillium italicum
                                                                                                                                                                                                                                                                                                LENGTH: 515
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             433
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                                                                  LLLLPSLLSLLLELILLKRRNRKTRENLPPGKSGW-PFLGETIGY-LKPYTATTLGDFMQ 69
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QHVSKYGKIYRSNLFGEPTIVSADAGLNRFILQNEGRLFECSYPRSIGGILGKWSMLVLV 129
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 LFNPWRWQQQNNGASSSGSGSFSTWGNNYMPFGGGPRLCAGSELAKLEMAVFIHHLVLKF 483
                                          LFLVSIVLNVIKQLIFYNRKE-----PPVVFHWIPFIGSTIAYGMDPY-----QFFF 67
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             NWELAEDDQ--PFAFPFVDFPNGLPIRVSRI 512
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   VLKSVTD----MVDKWSDKLSENGEVEVDVYEWFQILTEDVISRTAFGSSYEDGRAVFRL
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                                                                                                                                     Conservative
                                                                                                                                                      9.4%;
                                                                                                                                   ; Score 251; DB 10;
; Pred. No. 1.8e-12;
75; Mismatches 213;
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TITLE OF INVENTION: NUCLEIC ACIDS AND THERAPEUTIC AND SCREENING M.
TITLE OF INVENTION: RELATIG TO SAME
FILE REFERENCE: Attorney Docket No. US20020052031A1 1242-17
CURRENT APPLICATION NUMBER: US/09/909,903
CURRENT FILING DATE: 2001-07-20
NUMBER OF SEQ ID NOS: 21
SOFTWARE: PATENTIN VET. 2.1
SOFTWARE: PATENTIN VET. 2.1
SEQ ID NO 19
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ORGANISM: Penicillium italicum
US-09-909-903-19
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Patent No. US/00/20052031A1
GENERAL INFORMATION:
APPLICANT: Waterman, Michael R.
APPLICANT: Bellamine, Aouatef
                                                                                                                                                                                                                                                                                                                                                                                      Query Match 9.4%; Score 251; DB 10; Best Local Similarity 22.7%; Pred. No. 1.8e-12; Matches 120; Conservative 75; Mismatches 213;
                                                                182
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                   176 TIDLAAAMAEITIFTAARTLQ----GEEVRSKLTSEFADLFHDLDLGFSPINFMLPWAPL 231
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                                                                                                                                                                                                                                                                                                                        12 LLLLPSLLSLLLFLILLKRRNRKTRENLPPGKSGW-PELGETIGY-LKPYTATTLGDFMQ 69
                                                                                                                                                                                                                                                                                           21 LFLVSIVLNVIKQLIFYNRKE------PPVVFHWIPFIGSTIAYGMDPY-----QFFF 67
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    8
                                                             -----KFTENLMAKHIMSMDPGEEETEQLKKEY------VTFMKGVVSA 219
                                                                                                                                                      GDMHRDMRSISL----NFLSHARLRTILLKDVERHTLFVLDSWQQNSIFSAQDEAK----
                                                                                                                                                                                                   ASRAKYGDIFTFILLGKKTTVYLGVEGNEFIL--NGKLKDVNAEE----VYGKLTTPVFG
                                                                                                                                                                                                                                              QHVSKYGKIYRSNLFGEPTIVSADAGLNRFILQNEGRLFECSYPRSIGGILGKWSMLVLV
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   SSSGSGSFSTWGNNYMPFGGGPRLCAGSELAKLEMAVFIHHLVLKFNW
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                                                                                                        SDVVYDCPNSKLMEQKKFIKYGLSQEAL----ESYVPLIAD--ETNAYIKSSPNFKGQSG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              MPVPGTDFVVPPSHTLLSSPGVTARDERHFRDPLRWDPHRWESRVEVEDSSDTVDYGYGA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            PHNASAIKHTTYARDLSGNYPSATGSWRRRQRRRQD--------
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Sequence 8, Application US/10067668

Publication No. US20030022334A1

GENERAL INFORMATION:
APPLICANT: Glucksmann, Maria Alexandra
TITLE OF INVENTION: CYTOCHROME P450 FAMILY MEMBERS AND
FILE REFERENCE: 10448-136001

FILE REFERENCE: 10448-136001

CURRENT APPLICATION NUMBER: US/10/067,668

CURRENT FILING DATE: 2002-02-04

PRIOR APPLICATION NUMBER: 60/266,140

PRIOR APPLICATION NUMBER: 00/260,140

PRIOR FILING DATE: 2001-02-02

NUMBER OF SEQ ID NOS: 12

SOFTWARE: FastSEQ for Windows Version 4.0

SEQ ID NO 8

LENGTH: 544
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                                                                                            EMSKSDHYRKQRTDDDLLGWYLKHSNLSTEQILDLILSLLFAGHETSSVAIALAIFFLQA
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 NPDVQEKVHEEIERVIGANR-----APSLTDKAQMPYTEATIMEVQRLTVVVPLAIPHMT
                                  CPKAVEELREEHLEIARAKKELGESELNWDDYKKMDFTQCVINETLRLGNVVRF-LHRKA
                                                                                                                                                QVLLVNICPWLYYLPFGPFKELRQIEKDITSFL-----KKIIKDHQESLDRENPQDFI
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                                                                       DMYLL-HMEEERKNN-----SNSSFDEEYLFYIIGDLFIAGTDTTTNSLLWCLLYMSL
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NUMBER OF SEQ ID NOS: 21
SOFTWARE: Patentin Ver. 2.1
SEQ ID NO 18
LENGTH: 503
TYPE: PRT
ORGANISM: Homo sapiens
US-09-796-138-18
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Query Match
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TITLE OF INVENTION: MYCODACTERIUM tuberculosis CYP51 HIGH RESOLUTION STUCTURE,
TITLE OF INVENTION: NUCLEIC ACIDS, AND THERAPEUTIC AND SCREENING METHODS
TITLE OF INVENTION: RELATING TO SAME
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            CURRENT FILING DATE: 2001-02-28
PRIOR APPLICATION NUMBER: 09/345,218
PRIOR FILING DATE: 1999-06-30
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               FILE REFERENCE: Attorney Docket No. US20020031782A1 1242-17-2
CURRENT APPLICATION NUMBER: US/09/796,138
CURRENT FILING DATE: 2001-02-28
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            APPLICANT: Waterman, Michael R. APPLICANT: Bellamine, Aouatef
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KGYDIPSGWKYL--PYISAVHLDN--SRYDQPNLFNPWRWQQQNNGASSSGSGSFSTWGN
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                                                                                                                                          --DDILQTLLDATYKDGRPLTDDEVAGMLIGLLLAGQHTSSTTSAWMGFFL-ARDKTLQ-
                                                                                                                                                                           TDDDLLGWVLKHS-----NLSTEQILDLILSLLFAGHETSSVAIALAIFFLQACPKAVEE
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                                                                                                                                                                                                                                                                                                    EKNVFEALSE----LIILTASHCLH----GKEIRSQLNEKVAQLYADLDGGFSHAAWLLPG
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                                                              -KKCYLE---QKTVCGENLPPLTYDQLKDLNLLDRCIKETLRLRPPIMIMMRMARTPQTV 390
                                                                                                 LREEHLEIARAKKELGES--ELNWDDYKKMDFTQCVINETLRLGNVVRFLHRKALKDVRY
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Sequence 18, Application US/0909903

Patent No. US20020052031A1

GENERAL INFORMATION:
APPLICANT: Waterman, Michael R.
APPLICANT: Waterman, Michael R.
APPLICANT: Waterman, Michael R.
TITLE OF INVENTION: MYCOBacterium tuberculosis CYP51 POLYPEPTIDES AND TITLE OF INVENTION: NUCLEIC ACIDS AND THERAPEUTIC AND SCREENING METHODS

TITLE OF INVENTION: RELATING TO SAME
FILE REFERENCE: Attorney Docket No. US20020052031A1 1242-17

CURRENT APPLICATION (NUMBER: US/09/909,903

CURRENT FILING DATE: 2001-07-20

NUMBER OF SEQ ID NO.18

SEQ ID NO.18

LENCTH: 503

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ORGANISM: Homo sapiens
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181 KP 181 KR 241 F1 241 F1 301 IL 301 IL	1 M 1 M 61 A 61 A 61 A 121 G 121 G	Keywords: h 308-484/Dom 462/Binding Query Match Best Local Matches 51	A; Accession: T4614 32 A; Accession: T4614 32 A; Status: preliminary A; Molecule type: DNA A; Residues: 1-513 <blo 182="" 2;="" 3="" 74="" a;="" c;="" cross="" em="" experimental="" genetics:="" introns:="" map="" matprosition:="" note:="" position:="" references:="" source:="" t385.40<="" td=""><td>RESULT 1 T46143 Steroid 22-alpha-hydro N;Alternate names: pro C;Species: Arabidopsis C;Date: 04-Feb-2000 # C;Accession: T46143 R;Bloecker, H; Mewes, Submitted to the Prote</td><td>34 35 36 38 38 38 38 38 38 38 44 30 30 44 30 30 44 30 42 30 42 30 42 30 42 30 42 42 42 42 42 42 42 42 42 42 42 42 42</td></blo>	RESULT 1 T46143 Steroid 22-alpha-hydro N;Alternate names: pro C;Species: Arabidopsis C;Date: 04-Feb-2000 # C;Accession: T46143 R;Bloecker, H; Mewes, Submitted to the Prote	34 35 36 38 38 38 38 38 38 38 44 30 30 44 30 30 44 30 42 30 42 30 42 30 42 30 42 42 42 42 42 42 42 42 42 42 42 42 42
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MAKHIMSMI	TLLPLLLL	Superiamily: Synechocystis Keywords: heme; iron; metal 308-484/Domain: cytochrome 462/Binding site: heme iron Query Match 99. Best Local Similarity 99. Matches 512; Conservative	Accession: T46143 Accession: T46143 Status: preliminary Molecule type: DNA Residues: 1-513 <blo> Cross references: EMBL: ALI32979 Experimental source: cultivar Columbia; Genetics: Map position: 3 Introns: 74/2; 182/3; 233/3; 338/3; 369 Mote: T3A5.40</blo>	RESULT 1 T46143 Steroid 22-alpha-hydroxylase (DWF4) - 1 N;Alternate names: protein T3A5.40 C;Species: Arabidopsis thaliana (mouse- C;Date: 04-Feb-2000 #sequence_revision C;Accession: T46143 R;Bloecker, H.; Mewes, H.W.; Mayer, K.E submitted to the Protein Sequence Datah	11.0 11.0 10.9 10.9 10.8 10.8 10.7 10.7 10.7
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TEQ TEQ TEQ EVK	NET NET NET	Cyg Cyg	979 r C	DWF 5.4 a ( rev aye	2422222424244
LKKEYVTFMKGVVSAPLI	FILILKRRNRKTRFNLPP 	Neywords: heme; iron; metalloprotein 308-484/Domain: cytochrome P450 homology cp45> 462/Binding site: heme iron (Cys) (axial ligand) #s Query Match Best Local Similarity 99.8%; Pred. No. 1.1e-165; Matches 512; Conservative 1; Mismatches 0;	ВА	IGNMENTS  \text{vrabidopsis}  ear cress}  04-Feb-2000  \text{vx.;} Lemcke  base, Decemb	D96672 D96672 T48140 O4RTPB S35666 A27491 T05246 A29410 AG1987 T24780 JC4702 S38534 T04735
	MFETEHHTLLPLLLPSLLSLLLFLILKRRNRKTRENLPPGKSGWPELGETIGYLKPYT	cytochrome tatus predic Length 513; Indels	r3A5	aliana text_change 16- text_chueller,	cytochrome p450 probable Cytochr flavonoid 3',5' cytochrome p450 cytochrome p450 cytochrome p450 lanosterol 14alpl cytochrome p450
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A;Gene: CYP90
C;Superfamily: Synechocystis cytochrome P450 slr0574; cytochrome P450 homology
C;Keywords: chromoprotein; electron transfer; heme; iron; metalloprotein; monooxygenase;
F;275-440/Domain: cytochrome P450 homology <P45>
F;418/Binding site: heme iron (Cys) (axial ligand) #status predicted
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A; Residues: 1-472 <SZE>
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R;Szekeres, M.;
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C;Species: Arabidopsis thaliana (mouse-ear cress)
C;Date: 10-Sep-1999 #sequence_revision 10-Sep-1999 #text_change
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                   LLLLPSLLSLLLFLILLKRRNRKTRFNLPPGKSGWPFLGETIGYLKPYTATTLGDFMQQH 71
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                                                                                     NETLRVANIIGGVFRRAMTDVEIKGYKIPKGWKVFSSFRAVHLDPNHFKDARTFNPWRWQ
                                                                                                    NETLRIGNVVRFLHRKALKDVRYKGYDIPSGWKVLPVISAVHLDNSRYDQPNLFNPWRWQ 431
                                                                                                                                             GYETTSTIMTLAVKFLTETPLALAQLKEEHEKIRAMKSD--SYSLEWSDYKSMPFTQCVV
                                                                                                                                                                        GHETSSVAIALAIFFLQACPKAVEELREEHLEIARAKKELGESELNWDDYKKMDFTQCVI 371
                                                                                                                                                                                                                     LMSFDPG-EWSESLRKEYLLVIEGFFSLPLPLFSTTYRKAIQAR-----RKVAEALT
                                                                                                                                                                                                                                                                                                                      LHKRMHSLTMSFANSSIIKDHLMLDIDRLVRFNLDSWSSRVLL--MEEAKKITFELTVKQ
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                                                                                                                                                                                                                                                                                                                                                                                              VSKYGKIYRSNLFGEPTIVSADAGLNRFILQNEGRLFECSYPRSIGGILGKWSMLVLVGD 131
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Pred. No. 7.5e-56;
9; Mismatches 171;
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               GGTRFCPGAELARLQIALFLHYFITTYKWTQLKEDRISFFPSARLVNGFKIQLNR
                               GGPRLCAGSELAKLEMAVFIHHLVLKFNWELAEDDQPFAFPFVDFPNGLPIRVSR
                                                                      GCFVVPFLSAVHLDESYYKESLSFNPWRWLDPETQQKRNWRTSP----
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A;Map position: 1
C;Superfamily: Synechocystis cytochrome P450 slr0574; cytochrome P450
C;Keywords: heme; iron; metalloprotein
{ F; 455/Binding site: heme iron (Cys) (axial ligand) #status predicted
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C. Accession: H96759
C. Accession: H96759
R. Theologis, A.; Ecker, J.R.; Palm, C.J.; Federspiel, N.A.; Kaul, S.; White, (Chin, C.W.; Chung, M.K.; Conn, L.; Conway, A.B.; Conway, A.R.; Creasy, T.H.; Chin, C.W.; Chung, M.K.; Liu, J.; Johnson-Hopson, C.; Khan, S.; Khaykin, A. Authors: Hunter, J.L.; Jenkins, J.; Johnson-Hopson, C.; Khan, S.; Khaykin, A. Authors: Hunter, J.L.; Jenkins, J.; Johnson-Hopson, C.; Khan, S.; Khaykin, C.A.; Li, J.H.; Li, X.; Liu, S.X.; Liu, Z.A.; Lucos, J.S.; Maiti, R. R. R. R. R. R. Rooney, T.; Rowley, D.; Sakano, H. R.; Authors: Salzberg, S.L.; Schwartz, J.R.; Shinn, P.; Southwick, A.M.; Sun, F. Ker, M.; Wu, D.; Yu, G.; Fraser, C.M.; Venter, J.C.; Davis, R.W. A; Title: Sequence and analysis of chromosome 1 of the plant Arabidopsis. A; Reference number: A86141; MUID: 21016719; PMID: 11130712
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probable steroid 22-alpha-hydroxylase T9L24.44 [imported] - Arabidopsis that C; Species: Arabidopsis thaliana (mouse-ear cress)
C; Date: 02-Mar-2001 #sequence_revision 02-Mar-2001 #text_change 02-Apr-2002
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               A; Molecule type: DNA
A; Residues: 1-512 <STO>
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                                                                                                                                                                                                  AGNGVLGRLLEEESLPNESMADFIINLLFAGNETTSKTMLFAVYFLTHCPKAMTQLLEEH
GWKVLPVISAVHLDNSRYDQPNLFNPWRW-----QQQNNGASSSGSGSFSTWGNNYMPFG
                                                                -----DRIAGGMITWQDYKTMDFTQCVIDETLRLGGIAIWLMREAKEDVSYQDYVIPK
                                                                                                                                                                                                                                        TDDDLLGWVLKHSNLSTEQILDLILSLLFAGHETSSVAIALAIFFLQACPKAVEELREEH 341
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Pred. No. 1.6e-
05; Mismatches
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R.; Marzia
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hypothetical protein F18022.190 - Arabidopsis thaliana (?Species: Arabidopsis thaliana (mouse-ear cress) C;Date: 20-Apr-2000 #sequence_revision 20-Apr-2000 #text_change 20-Apr-2000 C;Accession: T48613 R;Bevan, M.; Murphy, G.; Ridley, P.; Hudson, S.; Bancroft, I.; Mewes, H.W.; submitted to the Protein Sequence Database, April 2000
                                                                                                                                                         RESULT
T48613
A; Reference number: Z24493
A; Accession: T48613
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C; Keywords: heme; ir
F; 396/Binding site:
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A; Map position: 4
C; Superfamily: Synechocystis cytochrome P450 slr0574;
C: Kerwords: heme; iron; metalloprotein
1--- 'Arrial ligand') #st
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A; Residues: 1-457 <STO>
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A;Accession: D85429
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  R; anonymous, The European Union Arabidopsis Genome Sequencing Consortium, The Cold Nature 402, 769-777, 1999
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                                                                                                                                                                                                                                   IRVATV 445
                                                                                                                                                                                                                                                                        IRVSRI 512
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      IPNGSLGWPVIGETLNFIACGYSSRPVT-----FMDKRKSLYGKVFKTNIIGTPIIIST
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                                             I.; Mewes, H.W.; Rudd,
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A;Cross-references: EMBL:U54770; NID:g1421740; PIDN:AAB17070.1; PID:g1421741 A;Experimental source: strain GCR758 C;Genetics:
                                                                                                                                                                                                                             R;Bishop, G.J.; Harrison, K.; Jones, J.D. plant Cell 8, 959-969, 1996
A;Title: The tomato Dwarf gene isolated b
                                                                                                                                                                                                                                                                                   cytochrome P450 homolog - tomato
C:Species: Lycopersicon esculentum (tomato)
C:Date: 14-May-1999 #sequence_revision 14-May-1999
                                                                                                                                                       A; Molecule type: mRNA
A; Residues: 1-464 <BIS>
                                                                                                                                                                                                  A;Reference number: Z16181; MUID:96266705; PMID:8672892
                                                                                                  A;Gene: dwarf
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A;Residues: 1-382 <BEV>
A;Cross-references: EMBL:DB
A;Experimental source: cultivar Columbia; BAC clone F18022
C;Genetics:
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A; Introns: 31/2; 1
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                                                               ;Superfamily: Syr
;273-436/Domain:
         Matches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   GRLFECSYPRSIGGILGKWSMLVLVGDMHRDMRSISLNFLSHARLRTILLKDVERHTLFV 164
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  GWPFIGETISFFKPHRSDSIGTFLQQRVSRYGKVFKSNICGGKAVVSCDQELNMFILQNE 61
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        GWPFLGETIGYLKPYTATTLGDFMQQHVSKYGKIYRSNLFGEPTIVSADAGLNRFILQNE 104
                      Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Similarity
                                                            Synechocystis cytochrome P450 slr0574; in: cytochrome P450 homology <P45>
      Conservative
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                  Score 761.5; DB 2
Pred. No. 7.9e-42;
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Pred. No. 2.1e-45;
   Mismatches
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                            DB 2;
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12 LLLLPSLLSLLLFLILLKRRN--RKTRFNLPPGKSGWPFLGETIGYLKPYTATTLG-DFM

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A; Accession: T04444

A; Molecula - T04444

A; Molecula - T04444
                                                                                                      A;Introns: 67/2; 173/3; 302/3; 358/1; 393/3
A;Note: T18B16.200; T5K18.10
C;Superfamily: Synechocystis cytochrome P450 slr0574;
C:Keywords: chromoprotein; electron transfer; heme; in
                                                                                                                                                                                                                                                                                                                                         A; Molecule type: DNA
A; Residues: 1-457 <BEV>
A; Cross-references: EMBL; AL021687
                                                                                                                                                                                                                                                                                                                                                                                                                                     cytochrome P450 - Arabidopsis thaliana N;Alternate names: protein T18BL6.200; protein T5 N;Contains: oxidoreductase (EC 1.-.-.) C;Species: Arabidopsis thaliana (mouse-ear cress) C;Date: 30-Apr-1999 #sequence_revision 30-Apr-199 C;Accession: T04444; T05806 C;Accession: T04444; T05806 C;Accession: T04444; T05806
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                                                                                                                                                                                       A; Experimental source: cultivar Columbia; BAC C; Genetics:
                                                                                                                                                                                                                                                                 A; Reference number: Z15453
A; Accession: T05806
                                                                                                                                                                                                                                                                                            A; Experimental source: cultivar Columbia; BAC clone T18B16 R; Bevan, M.; Van Der Schueren, J.; Chuang, Y.J.; Voet, M.; submitted to the Protein Sequence Database, April 1998
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A: Residues: 131-457 <BEW>
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                                 Matches
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LLLPSLLSLLLFLILLKRRNRKTRFNLPPGKSGWPFLGETIGYLKPYTATTLGDFMQQHV 72
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                                                Similarity
                                Conservative
                                             23.6%;
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Pred. No. 1
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                                Mismatches
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                                             DB 2;
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                                                                                                                                                                                                     clone T5K18
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                                                                                                        4; cytochrome P450 homology
iron; monooxygenase; oxidoreductase
                                Indels
                                                                                                                                                                                                                                                                                                            Robben, J.; Volckaert,
                              56;
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                            Gaps
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                                         Query Match
Best Local S
Matches 153
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            PSILSLLLFLILLK-----RRNRKTRFNLPPGKSGWPFLGETIGYLKPYTATTLGDFMQ
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A; Map position: 2

A; Map position: 2

A; Introns: 80/2; 187/3; 238/3; 321/3; 351/3; 413/3; 453/2

A; Introns: 80/2; 187/3; 238/3; 321/3; 351/3; 413/3; 453/2

C; Superfamily: Synechocystis cytochrome P450 slr0574; cytochrome F:291-453/Domain: cytochrome P450 homology <P45>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      A;Status: translated from GB/EMBL/DDBJ
A;Molecule type: DNA
A;Residues: I-482 <ROU>
A;Cross references: EMBL:ACO05315; NID:g3461834; PID:g3461849
A;Experimental source: cultivar Columbia
R;Ein, X.; Kaul, S.; Rounsley, S.D.; Shea, T.P.; Benito, M.I.; Town, C.D.;
M.; Koo, H.; Moffat, K.S.; Cronin, L.A.; Shen, M.; Vanaken, S.E.; Umayam, L
euss, D.; Nierman, W.C.; White, O.; Eisen, J.A.; Salzberg, S.L.; Fraser, C.
Nature 402, 761-768, 1999
                                                                                                                                                                                                                                                                                                                                                                                                         A;Title: Sequence and analysis of chromosome 2 of the plant Arabidopsis thaliana. A;Reference number: A84420; MUID:20083487; PMID:10617197 A;Accession: D84692
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A;Description: Arabidopsis thaliana chromosome II BAC T9I4 genomic sequence.
A;Reference number: 214710
A;Accession: T02739
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A; Residues: 1-482 <STO>
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           Local Similarity
les 153; Conser
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           Conservative
                                                                                                                                                                                                                                           T914.17
                                                                                                                                                                                                                                                                                             GB:AE002093; NID:g3461849; PIDN:AAC33235.1; GSPDB:GN00139
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                                      22.8%;
29.8%;
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           101;
24-Mar-1999 #text_change 16-Feb-2001
        Indels
           68;
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  Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Fujii, C.
L.; Tallon
C.M.; Vente
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A:Map position: 4COP9-4G3845
C;Superfamily: Synechocystis cytochrome P450 slr0574; cytochrome P450
C;Keywords: chromoprotein; heme; iron; metalloprotein; oxidoreductase
F;433/Binding site: heme iron (Cys) (axial ligand) #status predicted
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A:Autbors: Mueller-Auer, S.; Silvey, M.; James, R.; Montfort, A.; Pons, A.; Puigdomenecherhoft, A.; Moores, T.; Jones, J.D.G.; Eneva, T.; Palme, K.; Benes, V.; Rechman, S.; Ans
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C71417
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                A; Title: Analysis of 1.9 Mb of contiguous sequence from A; Reference number: A71400; MUID:98121113; PMID:9461215
                                                                                                                                                                                                                                                                                                                              A;Gene: d13695c
                                                                                                                                                                                                                                                                                                                                                                                              A; Molecule type: DNA
A; Residues: 1-487 <BEV>
                                                                                                                                                                                                                                                                                                                                                                                                                                  A; Status: nucleic acid sequence not shown; translation not shown
                                                                                                                                                                                                                                                                                                                                                                                                                                                                 A;Reference number: A71400;
A;Accession: C71417
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             C;Date: 10-Sep-1999 #sequence_revision 10-Sep-1999 #text_change 16-Jun-2000
C;Accession: C71417
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                                                                                      SLLSLLLFLILLKRRNRKTRFNLPPGKSGWPFLGETIGYLKPYTATTLGDFMQQHVSKYG
                                        SLFLVKIFHWYYQWRNPKTNGKLPPGSMGFPFIGETFEFFKPHDALQFSTFIKDRVLRFF 62
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      DTRKMPLTTRVIQETLRAASVLSFTFREAVQDVEYDGYLIPKGWKVLPLFRRIHHSSEFF
-----KIYRSNLFGEPTIVSADAGLNRFILQNEGRLFECSYPRSIGGI-----LG
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              TTSFRWEVIGDEEGIQYGPFPVPKKGLPIRVTPI 482
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        DQPNLFNPWRWQQQNNGASSSGSGSFSTWGNNYMPFGGGPRLCAGSELAKLEMAVFIHHL 479
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              DYKKMDFTQCVINETLRLGNVVRFLHRKALKDVRYKGYDIPSGWKVLPVISAVHLDNSRY 419
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              IADNIIGVIFAATDTTASVLTWLLKYLHDHPNLLQEVSREQFSIRQKIKKE--NRRISWE 341
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          GPYHSTLKRLVQSSFMPSALRPTV--SHIELLVLQTLSSWTSQKSINTLEYMKRYAFDVA 193
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ILDLILSLLFAGHETSSVAIALAIFFLQACPKAVEELREEHLBI-ARAKKELGESELNWD 359
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ---IMSAFGDKEEPTTIDVIKLLYQRLERGYNSMPLDLPGTLFHKSMKARIELSEELRKV 250
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             AKHIMSMDPGEEE---TEQLKKEYVTFMKGVVSAPLNLPGTAYHKALQSRATILKFIERK 245
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     GDMHRDM-RSISLNFLSHARLRTILLKDVERHTLFVLDSWQQNSIFSAQDEAKKFTFNLM 188
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   TRONKYGDIFKTHILGCPCVMISSPEAARMYLVSKAHLFKPTYPPSKERMIGPEALFFHQ 135
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           QHVSKYGKIYRSNLFGEPTIVSADAGLNRFTLQNEGRLFECSYPRSIGGILGKWSMLVLV 129
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           PALITLTIVVVVVVLLFKWWLHWKEQRLRLPPGSMGLPYIGET---LRLYTENP-NSFFA
                                                                                                                                                                  Similarity
                                                                                                                                             Conservative
                                                                                                                                                             21.7%;
27.3%;
                                                                                                                                          100;
                                                                                                                                   Score 581; DB 1; Length 487;
Pred. No. 4e-30;
0; Mismatches 205; Indels
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        A;Title: Sequence and analysis of chromosome 2 of the plant Arabidopsis thaliana. A;Reference number: A84420; MUID:20083487; PMID:10617197
A;Accession: A84859
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             R;Lin, X.; Kaul, S.; Rounsley, S.D.; Shea, T.P.; Benito, M.I.; Town, C.D.; Fuji M.; Koo, H.; Moffat, K.S.; Cronin, L.A.; Shen, M.; VanAken, S.E.; Umayam, L.; Teuss, D.; Nierman, W.C.; White, O.; Eisen, J.A.; Salzberg, S.L.; Fraser, C.M.; Nature 402, 761-768, 1999
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   probable cytochrome P450 [imported] - Arabidopsis thaliana
C;Species: Arabidopsis thaliana (mouse-ear cress)
C;Date: 02-Feb-2001 #sequence_revision 02-Feb-2001 #text_change 23-Mar-2001
C;Accession: A84859
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                          A; Gene: At2g42850
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    A; Cross-references:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     A; Residues: 1-485 <STO>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         A; Molecule type:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             A; Status: preliminary
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                                                                                                                                                                                                                                                                                                                                            Query Match
                                                                                                                                                                                                                                                                                                      Matches
185 FNLMAKHI--MSMDPGEEETEQLKKEYVTFMKGVVSAPLNLPGTAYHKALQSRATILKFI
                                                     132
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           467 LAKLEMAVFIHHLVLKFNWELAEDDQPFAFPFVDFPNGLPIRVS 510
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                                                                                                                         72 EDFVNPRIIKHGNIFKTRIMGSPTIVVNGAEANRLILSNEFSLVVSSWPSSSVQLMGMNC 131
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                                                                                                                                                                                                                                                 12 LLLLPSLLSLLLFL-----ILLKRRNRKTRFNLPPGKSGWPFLGETIGYLKPYTAT-TL 64
                                                                                                                                                                                                                                                                                                                          Local
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                                                                               MLVLVGDMHRDMRSISLNFLSHARLRTILLKDVERHTLFVLDSWQQNSIFSAQDEAKKFT 184
                                                                                                                                                                 GDFMQQHVSKYGKIYRSNLFGEPTIVSADAGLNRFILQNEGRLFECSYPRSIGGILGKWS 124
                                                                                                                                                                                                             LCIAATISSTLFFFRKKHHRFITKKIQKKKK--LLPGEMGLPWIGETMDFYKAQKSNRVF
                                          IMAKQGEKHRVLRGIVANSLSYIGLESLIPKLCDTVKFHHETEWRGKEEISLYRSAKVLT
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         G-YPHIHFNSEKYEDPYAFNPWRWEGKDLGAIVS-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            PVISAVHLDNSRYDQPNLFNPWRWQQQNNGASSSGSGSFSTWGNNYMPFGGGPRLCAGSE
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                                                                                                                                                                                                                                                                                                      al Similarity
147; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   LGWVLKHSNLSTEQILDLILSLLFAGHETSSVAIALAIFFLQACPKAVEELREEHLEIAR
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            DNA
                                                                                                                                                                                                                                                                                                    Conservative 107;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    GB:AE002093; NID:g4512670; PIDN:AAD21724.1; GSPDB:GN00139
                                                                                                                                                                                                                                                                                                                     21.6%; Score 579.5; DB 28.8%; Pred. No. 5e-30;
                                                                                                                                                                                                                                                                                                 Mismatches
                                                                                                                                                                                                                                                                                                                                         DB 2;
                                                                                                                                                                                                                                                                                                 203;
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L.; Tallon,
L.M.; Venter
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Ritheologis, A.; Ecker, J.R.; Palm, C.J.; Federspiel, N.A.; Kaul, S.; White, O.; Alonso, Chin, C.W.; Chung, M.K.; Conn, L.; Conway, A.B.; Conway, A.R.; Creasy, T.H.; Dewar, K.; ansen, N.F.; Hughes, B.; Huizar, L.
Nature 408, 816-820, 2000
A.Authors: Hunter, J.L.; Jenkins, J.; Johnson-Hopson, C.; Khan, S.; Khaykin, E.; Kim, C. C.A.; Lil, J.H.; Lil, X.; Lin, X.; Liu, S.X.; Liu, Z.A.; Luros, J.S.; Maiti, R.; Marziali, Rizzo, M.; Rooney, T.; Rowley, D.; Sakano, H.
A.Authors: Salzberg, S.L.; Schwartz, J.R.; Shinn, P.; Southwick, A.M.; Sun, H.; Tallon, ker, M.; Mu, D.; Yu, G.; Fraser, C.M.; Venter, J.C.; Davis, R.W.
A.; Title: Sequence and analysis of chromosome 1 of the plant Arabidopsis.
A.; Reference number: A86141; MUID: 21016719; PMID: 11130712
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C;Species: Arabidopsis thaliana (mouse-ear cress)
C;Date: 02-Mar-2001 #sequence_revision 02-Mar-2001 #text_change 31-Mar-2001
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C; Superfamily: 9
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                                                                                                                                                                                                                                                                                                                                                                                                                                   A; Residues: 1-490 <STO>
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                 A; Status: preliminary
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 DNLLNVK----DED-----GKTLDDEEIIDVLLMYLNAGHESSGHTIMWATVFLQEHP
                              SKSDHVRKQRTDDDLLGWVLKHSNLSTEQILDLILSLLFAGHETSSVAIALAIFFLQACP 331
                                                                              EMKGVVSAPLNLPGTAYHKALQSRATILKFIERKMEERKLDIKEEDQEEEEVKTEDEAEM
                                                                                                                       TYIPYIEENVITVLDKWTKMGEFEFLTHLRKLTFRII-MYIFLSSESENVMDALEREYTA 217
                                                                                                                                                                                    TTSDTCRRVLTDDD-AFKPGWPTSTMELIGRKSFVGISFEEHKRLRRLTAAPVNGHEALS
                                                                                                                                                                                                                                                ENRHYLPPGDLGWPFIGNMLSFLRAFKTSDPDSFTRTLIKRYGPKGIYKAHMFGNPSIIV 99
                                                                                                                                                                                                                                                                             KTRENLPPGKSGWPFLGETIGYLKPYTATTLGDFMQQHVSKYGK--IYRSNLFGEPTIVS 91
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 KKMDFTQCVINETLRLGNVVRFLHRKALKDVRYKGYDIPSGWKYLPVISAVHLDNSRYDQ
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                                                                                                                                                                                                                                                                                                           al Similarity 28.6
133; Conservative
                                                                                                                                                                                                                                                                                                                                                                        Synechocystis cytochrome P450 slr0574;
                                                                                                                                                                                                                                                                                                                         21.6%;
                                                                                                                                                                                                                                                                                                             107;
                                                                                                                                                                                                                                                                                                           Score 579.5; I
Pred. No. 5e-30
07; Mismatches
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                                                            -NQRKQNILSNKKDML
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                                                                                                                                                                                                                                                                                                                                      Length 490;
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A; Accession: T48973
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Local Similarity
DDQPFAFPFVDFPNGLPIRVSR
                                                                                                                                                                                                                                                                                                             FMKGV----
                              WEGKELRAGS -
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          145;
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511
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A;Gene: ATSP:F14D17.40
A;Map position: 3
A;Introns: 70/2; 178/3; 229/3; 312/3; 343/3; 346/1; 381/3
C;Superfamily: Synechocystis cytochrome P450 slr0574; cytochrome P450
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       A; Molecule type: DNA
A; Residues: 1-455 < GOR>
A; Cross-references: EMBL: AL353992; GSPDB: GN00061; ATSP: F14D17.40
A; Experimental source: cultivar Columbia; BAC clone F14D17
C; Genetics:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 cytochrome P450-like protein - Arabidopsis thaliana N;Alternate names: protein F14D17.40 C;Species: Arabidopsis thaliana (mouse-ear cress) C;Date: 02-Jun-2000 #sequence_revision 02-Jun-2000 #text_change 18-Aug-2000 C;Accession: T48973
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             R; Jordan, N.; Bangert, S.; Wiedelmann, R.; Voss, I submitted to the Protein Sequence Database, April
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           148 KILKDMDRVTREHLSSKAKTGRLDVKDAVSKLIIAHLTPKMMS------NLKPQTQA 198
                                                                                                                                        VINETLRLGNVVRFLHRKALKDVRYKGYDIPSGWKVLPVISAVHLDNSRYDQPNLFNPWR
                                                                                                                                                                                                                                                      AGHETSSVAIALAIFFLQACPKAVEELREEHLEIARAKKELGESELNWDDYK-KMDFTQC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ADAGLNRFILQNEGRLFECSYPRSIGGILGKWSMLVLVGDMHRDMRSISLNFLSHARLRT 151
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         NRKTRFNLPPGKSGWPFLGETIGYLKPYTATTLGDFMQQHVSKYGKIYRSNLFGEPTIVS
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                                                 WQQQNNGASSSGSGSFSTWGNNYMPFGGGPRLCAGSELAKLEMAVFIHHLVLKFNWELAE
                                                                                                                                                                                                                      VTQDTTSKAICLAVKFLLENPKVLAELKKEH-EVILESREDKEGGVTWEEYRHKMTFTN- 342
                                                                                                                                                                                                                                                                                                                                                                                      EDQEEEEVKTEDEAEMSKSDHVRKQRTDDDLLGWVLKHSN----LSTEQILDLILSLLF
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     NPKSNGKLPPGSMGFPIIGETLDFFKPYGFYEISPYLKKKMLRYGPLFRTNILGVKTVVS
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       -VSAPLNLPGTAYHKALQSRATILK--FIERKMEERKLDIKE
KTFMVFGTGLRQCAGAEFARLQISVFLHHLVTTYNFSLHQ
                                                                                                           --- MKSGYTIPAGWIVMIIPSVVHFDPEIYENPEENPWR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Score 577; DB 2;
Pred. No. 6.6e-30;
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                                                                                                                                                                                                                                                                                                                                    DDFLNTAIEESEKAGELLNENAIITLIFTLSC
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A;Title: Sequence and analysis of chromosome 2 of the plant Arabidopsis thaliana. A;Reference number: A84420; MUID:20083487; PMID:10617197
A;Recession: B84733
A;Status: preliminary
A;Molecule type: DNA
A;Residues: 1-489 <STO>
A;Cross-references: GB:AE002093; NID:g3831452; PIDN:AAC69934.1; GSPDB:GN00139
A;Cross-references: GB:AE002093; NID:g3831452; PIDN:AAC69934.1; GSPDB:GN00139
A;Genetics:
A;Geneti
RESULT 14
D96813
D96813
hypothetical protein T30F21.17 [imported] - Arabidopsis thaliana C:Species: Arabidopsis thaliana (mouse-ear cress)
C:Date: 02-Mar-2001 #sequence_revision 02-Mar-2001 #text_change C:Accession: D96813
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C;Species: Arabidopsis thallana (mouse-ear cress)
C;Date: 02-Feb-2001 #sequence_revision 02-Feb-2001 #text_change 16-Feb-2001
C;Accession: B84733
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Pred. No. 5.9e-28;
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Nature 408, 816-820, 2000
A;Authors: Hunter, J.L.; Jenkins, J.; Johnson-Hopson, C.; Khan, S.; Khaykin, E.; C.A.; Li, J.H.; Li, Y.; Lin, S.X.; Liu, S.X.; Liu, Z.A.; Luros, J.S.; Maiti, R.; Ma Rizzo, M.; Rooney, T.; Rowley, D.; Sakano, H.
A;Authors: Salzberg, S.L.; Schwartz, J.R.; Shinn, P.; Southwick, A.M.; Sun, H.; T.
A;Authors: Salzberg, S.L.; Schwartz, J.R.; Shinn, P.; Southwick, A.M.; Sun, H.; T.
A;Title: Sequence and analysis of chromosome 1 of the plant Arabidopsis.
A;Reference number: A86141; MUID:1016719; PMID:11130712
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A; Residues: 1-460 <STO>
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          13 LLLPSLLSLLLFLILLKRRNRKTRFNLPPGKSGWPFLGETIGYLKPYTATTLGDFMQQHV
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Local
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                                                                                                                                                                                                                                                                                                                                         LLFAGHETSSVAIALAIFFLQACPKAVEELREEHLEIARAKKELGESELNWDDYK-KMDF
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   MSMDPGEEETEQLKKEYVTFMKGVVSAPLNLPGTAYHKALQSRATILKFIERKMEERKLD
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                                                                FSMVQDSEIIRSPFHQYTKDLLINISQ
                                                                                                                                                                                       NPWRWQQQNNGASSSGSGSFSTWGN-NYMPFGGGPRLCAGSELAKLEMAVFIHHLVLKFN
                                                                                                                                                                                                                                   TNMVSNEVLRLANTTPLLFRKAVQDVEIKGKY-
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                                                                                                       WELAEDDQPFAFPFVDFPNGLPIRVSR
                                                                                                                                                 --WLWQ-----
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                                                                                                                                                                                                                                                                                                                     LAFALREGTSSCTALAVKFISKDPKVLAELKREHKAIVDNRKD-KEAGVSWEEYRHNMTF
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                                                                                                                                                 -GKEMIWGSKTFMAFGYGVRLCVGAEFSRLQMAIFLHHLVAYYD
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C;Accession: T02263

10-Sep-1999 #text\_change

21-Jul-2000

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R;Winkler, R.G.; Helentjaris, T.
Plant Cell 7, 1307-1317, 1995
A;Title: The maize dwarf3 gene encodes a cytochrome P450-mediated A;Reference number: Z14648; MUID:96004534; PMID:7549486

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A;Accession: T02263
A;Status: preliminary; translated from GB/EMBL/DDBJ
A;Molecule type: mRNA
A;Residues: 1-519 < WAIN>
A;Cross-references: EMBL:U32579; NID:g987266; PIDN:AAC49067.1; PID:g987267
A;Cross-references: EMBL:U32579; NID:g987266; PIDN:AAC49067.1; PID:g987267
A;Experimental source: strain B73
C;Gene:idvarf3
C;Gene: dwarf3
C;Function:
A;Gene: dwarf3
C;Function: involved in an early step in gibberellin biosynthesis
A;Description: involved in an early step in gibberellin biosynthesis
A;Rathway: gibberellin biosynthesis
C;Superfamily: Synechocystis cytochrome P450 slr0574; cytochrome P450 homology
C;Keywords: oxidoreductase
F;325-488/Domain: cytochrome P450 homology <P45>
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                                                                                                                                                                                                                                                                                                                                                                                      266 EDEAEMSKSDHYRKQRTDDDLLGWYLKHSNLSTEQILDLILSLLFAGHETSSVAIALAIF 325
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                                                                                                                                                                                                      RKALKDVRYKGYDIPSGWKVLPVISAVHLDNSRYDQPNLFNPWRWQQQNNGASSSGSGSF 445
                                                                                                                                                                                                                                                                                                                                                                                                                                                                               FMKGVVSAPLNLPGTAYHKALQSRATILKFIERKMEERKLDIKE-----EDQEEEEVKT 265
                                                                                      QDE------RGRHLDDD------EIIDVLVMYLNAGHESSGHITMWATV 342
                                                                                                                                                                                                                                                                   FLQENPDMFARAKAEQEAIMRSIPS-SQRGLTLRDFRKMEYLSQVIDETLRLVNISFVSF 401
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                                                                                                                                                                             RQATRDVFVNGYLIPKGWKVQLWYRSVHMDPQVYPDPTKFDPSRWE-----GHSPRAGTF 456
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    RARLPPGEMGWPLVGGMWAFLRAFKSGKPDAFIASFVRRFGRTGVYRSFMFSSPTVLVTT 128
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   SwissProt_40:*
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              C26A_HUMAN
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CP35_MOUSE
YRV1_CAEEL
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CP46_MESAU
CP60_RAT
CP59_MOUSE
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3 xenopus lae
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Query Match Best Local Similarity

36.5%; 41.9%;

Score 978.5; DB 1; Pred. No. 1.7e-51;

Length 472;

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STANDARD; PRT;  1. 37, Created) 1. 37, Last sequence; 1. 40, Last annotation 90A1 (EC 1.14) 0 OR CPD OR AT5G05690 11 ana (Mouse-ear cress; diplantae; Streptophy Magnoliophyta; eudico assicales; Brassicace; ;  A. A. Bassicales; Brassicace; ;  PubMed-8612270; 9; PubMed-8612270; 9; PubMed-8612270; nbia; nci G.P., Nagy F., Sch ds rescue the deficiel elongation and de-e; (1996).  A. B.	502 502 502 502 504 504 513
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Matches

79;

Mismatches

171;

Indels

41;

Gaps

8;

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RESULT 2
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C9M66; 023242;
16-OCT-2001 (Rel. 40, Created)
16-OCT-2001 (Rel. 40, Last sequence update)
15-JUN-2002 (Rel. 41, Last annotation update)
15-JUN-2002 (Rel. 41, Last annotation update)
Cytochrome P450 90C1 (EC 1.14.-.) (ROTUNDIFOLIA3).

ROT3 OR CYP9OC1 OR AT4G36380 OR C7A10 980 OR F23E13.220.

Arabidopsis thaliana (Mouse-ear cress).
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; Roside eurosids II; Brassicales; Brassicaceae; Arabidopsis.
                                             Mayer K.F.X., Schueller C., Wambutt R., Murphy G., Volckaert G., Pohl T., Duesterhoeft A., Stiekema W., Entlan K.-D., Terryn N., Harris B., Ansorge W., Brandt P., Grivell L.A., Rieger M., Mueller M., Weichselgartner M., de Simone V., Obermaier B., Mache R., Mueller M., Kreis M., Delseny M., Puigdomenech P., Watson M., Schmidtheini T., Kreis M., Delseny M., Puigdomenech P., Watson M., Schmidtheini T.,
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                                                                                                                                        MEDLINE-20083488; PubMed-10617198;
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H
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                                  Kreis M., Del
Reichert B.,
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                                                                                                                                                                                                               C-T., Tsukaya H., Uchimiya H.;
ROTUNDIFOLIA3 gene of Arabidopsis thaliana
e cytochrome P-450 family that is required
elongation of leaf cells.";
Dev. 12:2381-2391(1998).
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S. -A.,
                 Hoheisel J.,
             Portetelle D., Perez-Alonso M., Boutry M., Bancroft isel J., Zimmermann W., Wedler H., Ridley P.,
McCullagh B.,
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24

FLIL-

Matches

186;

Conservative

96;

Pred. No. 1.3e ; Mismatches

-LPPGKSGWPFLGETIGYL---

56

Indels

78;

Gaps

10

Similarity

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RA Bracken M., Weltjens I., Voet M., Bastlaens I., Aart K., Defoor E., RA Weltzenegger T., Bothe G., Ramsperger U., Hilbert H., Braun M., RA HOlzer E., Brandt A., Peters S., van Staveren M., Dirkse W., RA Holzer E., Brandt A., Peters S., van Staveren M., Dirkse W., RA Mooijman P., Klein Lankhorst R., Rose M., Hauf J., Koetter P., RA Berneiser S., Hempel S., Feldpausch M., Lamberth S., Van den Daele H., RA De Keyser A., Buysshaert C., Gielen J., Villarroel R., De Clercq R., RA Clark L., Doggett J., Hall S., Kay M., Lennard N., McLay K., Mayes R., RA Clark L., Doggett J., Hall S., Kay M., Lennard N., McLay K., Mayes R., RA Clark L., Doggett J., Hall S., Kay M., Lennard N., McLay K., Mayes R., RA Clark L., Doggett J., Hall S., Kay M., Lennard N., McLay K., Mayes R., Clark C., Doggett J., Harse A.C., Schaefer M., Meller-Auer S., Ra Dose S., de Haan M., Maarse A.C., Schaefer M., Meller-Auer S., RA Borkova D., Bloecker H., Scharfe M., Grimm M., Loehnert T.-H., RA Messenet O., Quigley F., Clabauld G., Muendlein A., Felber R., RA Gabel C., Fuchs M., Fartmann B., Granderath K., Dauner D., Herzl A., RA Massenet O., Quigley F., Clabauld G., Muendlein A., Felber R., RA Gibbons T., Weber N., Vandembol M., Bargues M., Terol J., Torres A., RA Gibbons T., Weber N., Vandembol M., Bargues M., Terol J., Torres A., RA Gibbons T., Weber N., Vandembol M., Bargues M., Terol J., Torres A., RA Frishman D., Haase D., Lemcke K., Mewes H.-W., Stocker S., Francs P., Bielke C., RA Frishman D., Haase D., Lemcke K., Mewes H.-W., Stocker S., Francs P., Bielke C., RA Frishman D., Barghei L., Condes M., Abu-Threideh J., Schutz K., Johnson D., Ra Kramer J., Fulton B., Miller N., Greco T., Kemp K., RA Schnich J., Wardis E., Dante M., Pepin K., Hillier L., Ra Ra Schnich J., Wardis E., Dante M., Pepin K., Hillier L., Ra Ra Schnich J., Wardis E., Dante M., Pepin K., Hillier L., Ra Chen E., March A., Shah R., Volone K., Coht M., Johnson A., Shah R., Schutz M., Johnson A., Shah R., Volone M., Johnson A., Shah R., Washa M., Johnson A., Marcha A., Shah R
                                                                                                                      BINDING
CONFLICT
                                                                                                                                                                                                             Oxidoreductase; Monooxygenase; Transmembrane; Endoplasmic reticulum; Multigene family.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          use by non-profit institutions as long modified and this statement is not removed. entitles requires a license agreement (See or send an email to license@isb-slb.ch).
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                                                                                             SEQUENCE
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                                                                                                                                                                                                                                                                                                                                          Pfam; PF00067;
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-I- FUNCTION: MIGHT BE INVOLVED IN THE BIOSYNTHESIS OF IMPORTANT FOR THE POLAR ELONGATION OF CELLS DURING-I-- SUBCELLULAR LOCATION: Membrane-bound. Endoplasmic in the control of the control
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Braeken M., Weltjens I., Voet M., Bastiaens
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L; AL161589; CAB80304.1; ALT_INIT.
L; Z97708; CAB16850.1; ALT_INIT.
L; Z94714; CAB16850.1; ALT_SEQ.
L; AL022141; CAB18139.1; ALT_SEQ.
erPro; IPR001128; Cytochrome_P450.
m; PF00067; p450; 1.
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15-DEC-1998 (Rel. 37, Created)
15-DEC-1998 (Rel. 37, Last sequence update)
15-DEC-1998 (Rel. 37, Last annotation update)
Cytochrome P450 85 (EC 1.14.-.-) (Dwarf protein).
                                                                                                                                                                                                                                                                                                         Bishop G.J., Harrison K., Jones J.J.G.D.;
"The tomato Dwarf gene isolated by heterologous transposon tagging encodes the first member of a new cytochrome P450 family.";
Plant Cell 8:959-969(1996).
-!- SIMILARITY: BELONGS TO THE CYTOCHROME P450 FAMILY.
                                                                                                                             the European Bloinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; Spermatophyta; Solanales; Solanaceae; Solanum.
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Eukaryota; Viridiplantae; Strept
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                                         InterPro; IPR001128; Pfam; PF00067; p450;
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MEDLINE=96266705; PubMed=8672892;
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                                                                                        EMBL; U54770; AAB17070
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  CYTOCHROME_P450;
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                                                                 Cytochrome_P450
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BINDING 414 414 HEME (BY SIMILARITY).
SEQUENCE 464 AA; 53706 MW; D2B2lAAAB7B14E94 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           C883_ARATH
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STRAIN-cv. Columbia;

MEDLINE-21016719; pubmed-11130712;

Theologis A., Ecker J.R., Palm C.J., Federspiel N.A., Kaul S.,

Theologis A., Cone J.R., Palm C.J., Federspiel N.A., Kaul S.,

White O., Alonso J., Altafi H., Araujo R., Bowman C.L., Brooks S.Y.,

Buehler E., Chan A., Chao Q., Chen H., Cheuk R.F., Chin C.W.,

Chung M.K., Conn L., Conway A.B., Conway A.R., Creasy T.H., Dewar K.,

Chunn P., Etgu P., Feldblyum T.V., Feng J.-D., Fong B., Fujii C.Y.,

Gill J.E., Goldsmith A.D., Haas B., Hansen N.F., Hughes B., Huizar L.,

Hunter J.L., Jenkins J., Johnson-Hopson C., Khan S., Khaykin E.,

Kim C.J., Koo H.L., Kremenetskaia I., Kurtz D.B., Kwan A., Lam B.,

Langin-Hooper S., Lee A., Lee J.M., Lenz C.A., Li J.H., Li Y.-P.,

Lin X., Liu S.X., Liu Z.A., Luros J.S., Maiti R., Marziali A.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                            15-DEC-1998 (Rel. 37, Last sequence update)
16-OCT-2001 (Rel. 40, Last annotation update)
Cytochrome P450 88A3 (EC 1.14.--,)
CYP88A3 OR ATIGO5160 OR YUP8H12.33.
Arabidopsis thailana (Mouse-ear cress).
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnollophyta; eudicotyledons; core eudicots; Rosid;
eurosids II, Brassicales; Brassicaceae; Arabidopsis.
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Pred. No. 1.4e-38;
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                                                                    RESULT 5
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Best Local S
Matches 133
            CP26_BRARE
P79739;
15-DEC-1998
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Militscher J., Miranda M., Nguyen M., Nierman W.C., Osborne B.I., Pata G., Peterson J., Pham P.K., Rizzo M., Roomey T., Rowley D., Sakano H., Salzberg S.L., Schwartz J.R., Shinn P., Southwick A.M., Sun H., Tallon L.J., Tambunga G., Toriumi M.J., Town C.D., Utterback T., Van Aken S., Vaysberg M., Vysotskala V.S., Walker M., Wu D., Yu G., Fraser C.M., Venter J.C., Davis R.W.; "Sequence and analysis of chromosome 1 of the plant Arabidopsis
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Oxidoreductase; Monooxygenase; Transmembrane; Heme. TRANSMEM 6 26 POTENTIAL. BINDING 439 439 HEME (BY SIMILARITY).
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PRINTS; PR00385; P450.
PROSITE; PS00086; CYTOCHROME_P450; 1.
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-I- SIMILARITY: BELONGS TO THE CYTOCHROME P450 FAMILY.
  15-DEC-1998
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            SEQUENCE
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                                                                                                            FLPFGAGSHLCPGNDLAKLEISIFLHHFLLKYQVKRSNPECPVMY
                                                                                                                                       YMPFGGGPRLCAGSELAKLEMAVFIHHLVLKFNWELAEDDQPFAF
                                                                                                                                                                                          VRYKGYDIPSGWKVLPVISAVHLDNSRYDQPNLFNPWRWQQQNNGASSSGSGSFSTWGNN
                                                                                                                                                                                                                      EVIQRAKAEQEMILKSRPE-GQKGLSLKETRKMEFLSQVVDETLRVITFSLTAFREAKTD
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                                                                                                                                                                   VEMNGYLIPKGWKVLTWFRDVHIDPEVFPDPRKFDPARW----DNG-
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133; Conserv
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490 AA;
              (Rel.
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28.6%;
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There are no restrictions
ong as its content is in
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                                                                                           ALQSRATILKFIERKMEERKLDIKEEDQEEEEVKTEDEAEMSKSDHVRKQRTDDDLLGWV
                                                                                                                      CVLVYPEMKKLMFRIAMRILLGFEPEQIKTDEQELVEAFEEMIKNLFSLPIDVPFSGLYR
                                                                                                                                                                                           ILGKWSMLVLVGDMHRD-----MRSISLNFLSHARLRTILLKDVERHTLFVLDSW-QQNS 172
            ----PFSLQAMKEAATELLFGGHETTASTATSLVMFLGLNTEVVQKVREE-----VQEKVE
                                      LKHSNLSTEQILDLILSLLFAGHETSSVAIALAIFFLQACPKAVEELREEHLEIARAKKE
                                                                 GLRAR----IENSKIEENIRKKIQDDDNENEQKYKDALQLL----IENSRRSDE----
                                                                                                                                                 IFSAQDEAKKFTFNLMAKHIMSMDPGEEET--EQLKKEYVTFMKGVVSAPLNLPGTAYHK 230
                                                                                                                                                                            ILGSDTLSNVHGVQHKNKKKAIMRAFSRDALEH-----YIPVIQQEVKSAIQEWLQKDS 172
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                                                                                                                                                                                                                                                                                                                                                                                                 Endoplasmic reticulum BINDING 438 43
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          EMBL; U68234; AAC60045.1; -.
ZFIN; ZDB-GENE-990415-44; cyp26.
InterPro; IPR001128; Cytochrome_P450.
Pfam; PF00067; p450; 1.
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Hsu K.E., Dilworth F.J., Jones G., Petkovich M.;
"Identification of the retinoic acid-inducible all-trans-retinoic acid 4-hydroxylase.";
acid 4-hydroxylase.";
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Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Actinopterygii; Neopterygii; Teleostei; Ostariophysi; Cypriniformes;
Cyprinidae; Danio.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            15-DEC-1998 (Rel. 37, Last annotation update) Cytochrome P450 26 (EC 1.14.-.-) (Retinoic acid-metabolizing cytochrome) (P450RAI) (Retinoic acid 4-hydroxylase).
                                                                                                                                                                                                                                                                                                                                                                                                                                                   Oxidoreductase; Monooxygenase; Membrane; Heme;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     PRINTS; PR00385; P450 PROSITE; PS00086; CYT
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SUBCELLULAR LOCATION: Membrane-bound. Endoplasmic reticulum.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Biol. Chem. 271:29922-29927(1996). FUNCTION: PLAYS A KEY ROLE IN RET
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                                        YTATTLGDFMQQHVSKYGKIYRSNLFGEPTIVSADAGLNRFILQNEGRLFECSYPRSIGG
                                                                                                                      YTLMVTFLCTIVLPVLLFLAAVKLWEMLMIRRVDPNCRSPLPPGTMGLPFIGETLQLI-- 61
---LQRRKFLRMKRQKYGCIYKTHLFGNPTVRVMGADNVRQILLGEHKLVSVQWPASVRT 118
                                                                                                                                                                                                                                                                              Similarity
                                                                                                                                                                                                                                                                                                                                                               438
492 AA;
                                                                                                                                                                                                                                            Conservative
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27.6%;
                                                                                                                                                                                                                                               95;
                                                                                                                                                                                                                                         Score 503; DB
Pred. No. 3.8e
95; Mismatches
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Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                           This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its modified and this statement is not removed. Usage by and for commercial entitles requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
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15-DEC-1998 (Rel. 37, Last sequence update)
15-JUN-2002 (Rel. 41, Last annotation updat.
Cytochrome P450 88A1 (EC 1.14.-.-) (DWARF3 |
CYP88A1 OR D3.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Q43246;
15-DEC-1998
15-DEC-1998
15-JUN-2002
                                                                                                                                                                                                                                                                       BINDING
                                                                                                                                                                                                                                                                                     TRANSMEM
                                                                                                                                                                                                                                                                                                Oxidoreductase;
                                                                                                                                                                                                                                                                                                                               Pfam; PF00067; p450;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              <del>-</del>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              "The maize Dwarf3 gene encodes a cytochrome P450-mediated in Gibberellin biosynthesis."; Plant Cell 7:1307-1317(1995).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Eukaryota; Viridiplantae; Streptophyta; Espermatophyta; Magnoliophyta; Liliopsida; Panicoideae; Andropogoneae; Zea.
                  187
                                                                                                                                                                                                                                                                                                                                                InterPro;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     MAIZE
                                             153
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Winkler R.G., Helentjaris T.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           MEDLINE=96004534; PubMed=7549486;
                                                                            129
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       SEQUENCE FROM N.A.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   PATHWAY: Gibberellin biosynthesis; early step.
TISSUE SPECIFICITY: EXPRESSED IN ROOTS, DEVELOPING
VEGETATIVE MERISTEM, AND SUSPENSION CULTURE CELLS.
SIMILARITY: BELONGS TO THE CYTOCHROME P450 FAMILY.
                                                                                                                                             RFNLPPGKSGWPFLGETIGYLKPYTATTLGDFMQQHVSKYGK--IYRSNLFGEPTI-VSA 92
         YLPFIDRTVTSSLRAWADHGGSVEFLTELRRWTFKIIVQ-IFLGGADQATTRALERSYTE
                                  LLKDVERHTLFVLDSW-QQNSIFSAQDEAKKFTFNLMAKHIMSMDPGEEETEQLKKEYVT
                                                                   AEGCKQVLMDDDA--FVTGWPKATVALVGPRSFVAMPYDEHRRIRKLTAAPINGFDALTG
                                                                                             DAGLNRFILQNEGRLFECSYPRSIGGILGKWSMLVLVGDMHRDMRSISLNFLSHARLRTI 152
                                                                                                                           RARLPPGEMGWPLVGGMWAFLRAFKSGKPDAFIASFVRRFGRTGVYRSFMFSSPTVLVTT 128
                                                                                                                                                                                              129;
                                                                                                                                                                                                                                                                                                                                                           U32579; AAC49067.1;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         PVISAVHLDNSRYDQPNLFNPWRWQQQNNGASSGSGSFSTWGNNYMPFGGGPRLCAGSE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       MGMYTPGKGLSMELLDQLKYTGCVIKETLRINPPVPGGFRVALKTFELNGYQIPKGWNVI
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        LG----ESELNWDDYKKMDFTQCVINETLRLGNVVRFLHRKALKDVRYKGYDIPSGWKVL 406
                                                                                                                                                                                                                                                                                                                   PS00086;
                                                                                                                                                                                                                                                                                                                                             IPR001128;
                                                                                                                                                                                                                                                      466
519 /
                                                                                                                                                                                            Conservative
                                                                                                                                                                                                                                                      AA;
                                                                                                                                                                                                                                                                                Monooxygenase;
21 Pr
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                                                                                                                                                                                                                                                                                                              CYTOCHROME_P450; 1.
                                                                                                                                                                                                                                                    466 H
57906 MW;
                                                                                                                                                                                                     18.3%;
28.2%;
                                                                                                                                                                                                                                                                                                                                        Cytochrome_P450.
                                                                                                                                                                                           91;
                                                                                                                                                                                                                     Score 491.5;
                                                                                                                                                                                                       Pred.
                                                                                                                                                                                                                                                                               POTENTIAL.
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0F8977A024316D95 CRC64;
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                                                                                                                                                                                           Mismatches
                                                                                                                                                                                                         No.
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                                                                                                                                                                                                         2e-22;
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a; Poales; Poaceae; PACC cl
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ĀĀ
                                                                                                                                                                                                                     DB 1;
                                                                                                                                                                                         189;
                                                                                                                                                                                                                                                                                              Heme.
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                                   211
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C120_SYNY3
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                                                                                                                              the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Q59990;
16-OCT-2001
      SEQUENCE
                                                                                                                                                                                                                                                                          "Sequence analysis of the genome of the unicellular cyanobacterium Synechocystis sp. strain PCC6803. II. Sequence determination of the entire genome and assignment of potential protein-coding regions."
                                                                                                                                                                                                                                                                                                                                 Kaneko T., Sato S., Kotani H., Tanaka A., Asamizu E., Nakamura Y., Miyajima N., Hirosawa M., Sugiura M., Sasamoto S., Kimura T., Hosouchi T., Matsuno A., Muraki A., Nakazaki N., Naruo K., Okumura Shimpo S., Takeuchi C., Wada T., Watanabe A., Yamada M., Yasuda M.,
                               Complete proteome.
                                          PROSITE; PS00086; CYTOCHROME_P450; 1.
Hypothetical protein; Oxidoreductase;
                                                           Pfam; PF00067; p450; 1.
PROSITE; PS00086; CYTOCHROME_P450;
                                                                                                        EMBL; D64003; BAA10496.1;
                                                                                                                                                                                                                                                                                                                                                                                                 SEQUENCE FROM N.A. MEDLINE=97061201; PubMed=8905231;
                                                                                                                                                                                                                                                                                                                                                                                                                                               "Sequence analysis of the genome of the unicellular cyanobacterium synechocystis sp. strain PCC6803. I. Sequence features in the 1 Mb region from map positions 64% to 92% of the genome."; DNA Res. 2:153-166(1995).
                                                                                          InterPro;
                                                                                                                                                                                                                                                 DNA Res. 3:109-136(1996).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Synechocystis sp. (strain PCC 6803).
Bacteria; Cyanobacteria; Chroococcales; Synechocystis.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         16-OCT-2001 (Rel. 40, Created)
16-OCT-2001 (Rel. 40, Last sequence update)
16-OCT-2001 (Rel. 40, Last sequence update)
Putative cytochrome p450 120 (EC 1.14.-.-).
CYP120 OR CYP OR SLR0574.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Sugiura M., Tabata
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         MEDLINE=96127529; PubMed=8590279;
Kaneko T., Tanaka A., Sato S., Ko
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  NCBI_TaxID=1148;
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                                                                                       IPR001128; Cytochrome_P450
    444 AA;
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391 H
50578 MW;
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                 HEME
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 8F62A9EED3B54BDC
                  (BY
                                          Monooxygenase;
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Sazuka T.,

Miyajima

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EMBL outstation a collaboration

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RESULT 8
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Best Local Similarity
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                                                                                                                                                                                                                                                                                          CP26_MOUSE STANDARD; PRT; 497 AA.

055127; 09R1F4;
15-DEC-1998 (Rel. 37, Created)
15-DEC-1998 (Rel. 37, Last sequence update)
15-JUN-2002 (Rel. 41, Last annotation update)
Cytochrome P450 26 (EC 1.4.-.) (Retinoic acid-metabolizing cytochrome) (P450RAI) (Retinoic acid 4-hydroxylase).

CYP26AI OR CYP26 OR P450RA.
                                      MEDIJINE-98113212; PubMed-9442090;
MEDIJINE-98113212; PubMed-9442090;
Abu-Abed S.S., Beckett B.R., Chiba H., Chithalen J.V., Jones G.,
Metzger D., Chambon P., Petkovich M.;
Metzger D., Chambon P., Petkovich M.;
"Mouse P450RAI (CYP26) expression and retinoic acid-inducible retinoic acid metabolism in F9 cells are regulated by retinoic acid receptor gamma and retinoid X receptor alpha.";
J. Biol. Chem. 273:2409-2415(1998).
                                                                                                                                               "Metabolic inactivation of retinoic acid by a novel p450 differentially expressed in developing mouse embryos."; EMBO J. 16:4163-4173(1997).
                                                                                                                                                                                                                                                              Eukaryota; Metazoa; Chordata;
Mammalia; Eutheria; Rodentia;
                                                                                                                                                                                            Fujii H.,
                                                                                                                                                                                                                                                                                                                                                                                          MOUSE
   MEDLINE-20515038;
                       SEQUENCE FROM N.A.
                                                                                                                            SEQUENCE FROM
                                                                                                                                                                                   Kato
                                                                                                                                                                                                       MEDLINE-97392446; PubMed-9250660;
                                                                                                                                                                                                                     STRAIN-C3H
                                                                                                                                                                                                                               SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                      Mus musculus (Mouse).
                                                                                                                                                                                                                                                  NCBI_TaxID=10090;
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                                                                                                                                                                                   S., Hamada H.;
                                                                                                                                                                                                                                                                                                                                                                                                                                  ----HVPFGGGLRECLGKEFARLEMKLFATRLIQQFDWTL 416
                                                                                                                                                                                                                                                                                                                                                                                                                                                       TWGNNYMPFGGGPRLCAGSELAKLEMAVFIHHLVLKFNWEL
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         LGQHSDIRERVRQE-----QNKLQLSQ-ELTAETLKKMPYLDQVLQEVLRLIPPVGGGFR
                                                                                                                                                                                            Sato
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                                                                                                                           N.A.
   PubMed=11063033
                                                                                                                                                                                             Kaneko
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                                                                                                                                                                                            S., Gotoh O., Fujii-Kuriyama Y.,
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Pred. No. 8.5e-22;
                                                                                                                                                                                                                                                               Craniata; Vertebrata; Sciurognathi; Muridae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Mismatches
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; Murinae; Mus
                                                                                                                                                                                             Osawa
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AKKELGESELNWDDYKKMDFTQCVINETLRLGNVVRFLHRKALKDVRYKGYDIPSGWKVL
                                           LGWYLKHSNLSTEQILDLILSLLFAGHETSSVAIALAIFFLQACPKAVEELREEHLEIAR
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EMBL; Y12657; CAA73206.1; -.
EMBL; AF115769; AAD177217.1; -.
EMBL; BC012673; AAH12673.1; -.
HSSP; P14779; 1UPZ.
HGD; MGI:1096359; CYP26a1.
InterPro; IPR001128; Cytochrome_P450.
Pfam; PF00067; P450; 1.
PRINTS; PR00385; P450.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Paine C.T., Paine M.L., Snead M.L.;
"Identification of tuftelin- and amelogenin-interacting proteins using the yeast two-hybrid system.";
Connect. Tissue Res. 38:257-267(1998).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Oxidoreductase; Monooxygenase; Membrane; Heme;
                                                                                                                                                                                                                                                                                                                                                                                                                               10 LPLLLLPSL----LSLLLFLILLK------RRNRKTRFNLPPGKSGWPFLGETIGYLK 57
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            FUNCTION: Plays a key role in retinoic acid metabolism. Acts on retinoids, including all-trans-retinoic acid (RA) and its stereolsomer 9-cis-RA. Capable of both 4-hydroxylation and 18-hydroxylation. Responsible for generation of several hydroxylated forms of RA, including 4-OH-RA, 4-oxo-RA, AND 18-OH-RA. SUBCELLULAR LOCATION: Membrane-bound. Endoplasmic reticulum. INDUCTION: BY RETINOIC ACID.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   European Bioinformatics Institute.
                                                                                                                                                                                         TILGAGCLSNLHDSSHKQRKKVIMQAFSREALQCYVLV-IAEEVSSCLEQWLSCGERGLL
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                                                                                                                                                                                                                                                                                                                          PYTATTLGDFMQQHVSKYGKIYRSNLFGEPTIVSADAGLNRFILQNEGRLFECSYPRSIG 117
                                                                                                                                                                                                                                                                                                                                                                                   LPALLASALCTFVLPLLLFLAALKLWDLYCVSSRDRSCALPLPPGTMGFPFFGETL----
  VKARNLIHARIEENIRAKIRRLQATEPDGGCKDALQLLIEHSWE-----
                                                                                              VYPEVKRLMFRIAMRILLGCEPGPAGGGEDEQQLVEAFEEMTRNLFSLPIDVPFSGLYRG
                                                                                                                                     AQDEAKKFTFNLMAKHIMSMDPGE----EETEQLKKEYVTFMKGVVSAPLNLPGTAYHKA
                                                                                                                                                                                                                                        GILGKWSMLVLVGDMHRDMRSISLNFLSHARLRTILLKDVERHTLFVLDSWQQ--NSIFS 175
                                               LQSRATILKFIERKMEE---RKLDIKEED----QEEEEVKTEDEAEMSKSDHVRKQRTDDDL
                                                                                                                                                                                                                                                                                     -OMVLORRKFLOMKRRKYGFIYKTHLFGRPTVRVMGADNVRRILLGEHRLVSVHWPASVR 117
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148; Conserv
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28.4%;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   78;
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Pred. No. 1
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L -> P (IN REF. 4).
I -> T (IN REF. 4).
Y -> H (IN REF. 4).
33B07D7C29134471
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W REF. 4).
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-RGERLDMQ-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 64;
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C26A_HA

ID C26A_H

AC 09N63
DT 15-UNN
DT 15-U
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O9NR63; Q9NP41;
15-JUN-2002 (Rel. 41, Created)
15-JUN-2002 (Rel. 41, Last sequence update)
15-JUN-2002 (Rel. 41, Last annotation update)
Cytochrome P450 26A2 (EC 1.14.-.-) (P450RAI-2)
       CONFLICT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            MREDLINE=20300913; PubMed=10823918; White J.A., Ramshaw H., Talmi M., Stangle W., Zha White J.A., Ramshaw H., Talmi M., Stangle W., Zha Creighton S., Tam S.-P., Jones G., Petkovich M.; "Identification of the human cytochrome P450, P45 predominantly expressed in the adult cerebellum a all-trans-retinoic acid metabolism."; Proc. Natl. Acad. Sci. U.S.A. 97:6403-6408(2000).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Homo sapiens (Human).
Eukaryota; Metazoa; Chordata;
Mammalia; Eutheria; Primates;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 metabolizing cytochrome).
CYP26A2 OR P450RAI2.
                                                                                                                                                                                                                                                                                                       entities requires a license agreement (S or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                          modified and this statement is not removed. entities requires a license agreement (See
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             [2]
SEQUENCE FROM N.A.
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                                                    BINDING
                                                                         Endoplasmic reticulum
                                                                                        Oxidoreductase; Monooxygenase; Membrane;
                                                                                                                    PROSITE;
                                                                                                                                            Pfam; PF00067; p450; PRINTS; PR00385; P45
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         NCBI_TaxID=9606;
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                                                                                                                                                                                                                                                                                                                                                                       European Bioinformatics Institute. There are no rest
by non-profit institutions as long as its content
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 similarity).
TISSUE SPECIFICITY: Highly expressed in brain,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   INDUCTION: By retinoic acids (RA). SIMILARITY: BELONGS TO THE CYTOCHROME P450 FAMILY.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                cerebellum and pons
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     SUBCELLULAR LOCATION: Membrane-bound.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ENZYME REGULATION: Has a preferred activity towards substrates: all-trans-RA > 9-cis-RA > 13-cis-RA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        generation of several hydroxylated forms of RA, 4-oxo-RA, and 18-OH-RA.
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                                                                                                                                                                                                             605207
                                                                                                                                                                                                                                                                                                                                                                                                                     SWISS-PROT entry is copyright. It is produced through a collaboration -
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              FAKILLKIFTVELARHCDWQLLNGPPTMKTSPTVYPVDNLP
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                                                                                                                                                                                                                                AF252297; AAF76003.1;
AC007002; AAF65576.1;
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       68
512 ‡
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                                                                                                                    CYTOCHROME_P450;
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    68
57512
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    HEME (POTENTIAL).
Q -> QKCTLRETRVWLPQ
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Endoplasmic reticulum
                                                                                                                                                                                                                                                                                                                          http://www.isb-sib.ch/announce/
                                                                                                                                                                                                                                                                                                                                             Usage
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Best I
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                                                                                                                                      MEDLINE=99077803; PubMed=9857192; Hollemann T., Chen Y., Grung u
                                                                                                                                                                                                                                                          15-JUN-2002 (Rel. 41, Last sequence update)
15-JUN-2002 (Rel. 41, Last annotation update)
Cytochrome P450 26 (EC 1.14. --) (Retinoic acid degrading
CYP26) (XCYP26) (Retinoic acid converting enzyme) (RACE).
CYP26A1 OR CYP26.
          This
                                                                                                                                                                                                         Eukaryota; Metazoa; Chordata;
Amphibia; Batrachia; Anura; Mexenopodinae; Xenopus.
                                                                                                            EMBO
                                                                                                                                 "Regionalized metabolic
                                                                                                                                                                                                                                              Xenopus laevis (African clawed frog)
                                                                                                                                                                                                                                                                                                                                     093323;
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                                                                                              -!- FUNCTION: Plays a
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                                  SIMILARITY:
                                                                       SUBCELLULAR LOCATION:
                                                           similarity).
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                                                                                                           J. 17:7361-7372(1998).
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          SWISS-PROT entry is copyright.
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                                By retinoic acid.
BELONGS TO THE CYTOCHROME P450 FAMILY.
                                                                                                                                                                                                                                                                                                                                                 STANDARD;
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                                                                                                                                  activity
                                                                       Membrane-bound.
                                                                                               role
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                                                                                                                                                                                                                       Mesobatrachia;
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Pred. No. 9.
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establishes
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          It is produced through
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.9e-20;
                                                                       Endoplasmic
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a collaboration -
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RESULT 11
CP26_CHICK
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Best Local S
Matches 149
                                                                                                                           Q9PUB4; Q9PUG2;
15-JUN-2002 (Rel. 4
15-JUN-2002 (Rel. 4
15-JUN-2002 (Rel. 4
                                                      CYP26A1 OR CYP26.
Gallus gallus (Chicken).
Eukaryota; Metazoa; Chor
                                         Archosauria; Aves;
                                                                                                  CYP26)
                                                                                                              Cytochrome P450
NCBI_TaxID=9031;
                                                                                                                                                                                     CP26_CHICK
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Endoplasmic reticulum.
BINDING 437 437
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Pfam; PF00067; p450; 1. 
PRINTS; PR00385; P450. 
PROSITE; PS00086; CYTOCHROME_P450; 1.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   entities requires a license agreement
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                use by non-profit institutions as long modified and this statement is not removed.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            SEQUENCE
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                                                                                                                                                                                     STANDARD;
                                                                                                              26
                                                                                                          41, Created)
41, Last sequence update)
41, Last annotation update)
41, Last annotation update)
6 (BC 1.14.-.-) (Retinoic acid degrading
                                       Neognathae;
                                       Chordata; Craniata; Vertebrata; Euteleostomi;
Neognathae; Galliformes; Phasianidae; Phasiani
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   16.6%;
28.7%;
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                                       Phasianidae; Phasianinae;
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Matches 141;
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Submitted (SEP-1999) to the EMBL/GenBank/DDBJ databases.
-i- FUNCTION: Plays a key role in retinoic acid metabolism. Appears be involved in the specific inactivation of all-trans-RA.
Responsible for generation of several hydroxylated forms of RA,
including 4-0H-RA, 4-oxo-RA, and 18-0H-RA.
-i- SUBCELLULAR LOCATION: Membrane-bound. Endoplasmic reticulum.
-i- DEVELOPMENTAL STAGE: Expressed at stage 7 its expression
decreases in the anterior part of the embryo. From stage 7-10 it
expression is restricted to the dorsal folds of the neural tube.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                EMBL;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   This SWISS-PROT entry is copyright. It is produced through a collab between the Swiss Institute of Bioinformatics and the EMBL outst the European Bioinformatics Institute. There are no restrictions use by non-profit institutions as long as its content is in modified and this statement is not removed. Usage by and for comentities requires a license agreement (See http://www.isb-sib.ch/an or send an email to license@isb-sib.ch).
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MEDLINE-20057772; PubMed-10588879;
Swindell E.C., Thaller C., Sockana
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       SEQUENCE
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PROSITE; PS00086; CYTOCHROME_P450; 1.
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SIMILARITY: BELONGS TO THE CYTOCHROME P450 FAMILY.
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                                                  AYHKALQSRATILKFIERKMEERKLDIKEEDQEEEEVKTEDEAEMSKSDHVRKQRTDDDL
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PF00067; p450; 2.
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I -> V (IN REF. 2).
GPI -> SPT (IN REF. 2).
; 7F28B72E75C232FB CRC64;
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Pred. No. 2.:
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RESULT 12
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the Euro
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                                                                                                                                                                                                                                                                                                                                                                                                                                    White J.A., Beckett-Jones B., Guo Y.-D., Dilworth Jones G., Petkovich M.; Jones G., Petkovich M.; "CDNA cloning of human retinoic acid-metabolizing identifies a novel family of cytochromes P450."; J. Biol. Chem. 272:18538-18541(1997).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               15-DEC-1998 (Rel. 37, Created)
15-DEC-1998 (Rel. 37, Last sequence update)
16-OCT-2001 (Rel. 40, Last annotation update)
Cytochrome P450 26 (EC 1.14.--) (Retinoic cytochrome) (P450RAI) (hP450RAI) (Retinoic CYP26AI) OR CYP26.
               modified
                                                                                                                                                                                                                                                                                                                   Cell Growth Differ. 9:629-637(1998).
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MEDLINE-98380037; PubMed-9716180;
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                                       ween the Swiss Institute of Bioinformatics Institute.
                                                                                                                                                                                                                                                                                                                                 colon carcinoma cells."
                     SWISS-PROT entry is copyright. It is produced through a collaboration een the Swiss Institute of Bioinformatics and the EMBL outstation - European Bioinformatics Institute. There are no restrictions on its by non-profit institutions as long as its content is in no way
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agreement (See http://www.isb-sib.ch/announce/
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(Retinoic acid 4-hydroxylase)
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Best Local Similarity
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01-NOV-1997
30-MAY-2000
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SEQUENCE FROM N.A.
SEQUENCE FROM N.A.
                                                                   Eukaryota; Metazoa;
                                                                              Caenorhabditis elegans.
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PROSITE; PS00086; CYTC
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                                                                                                        cytochrome
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                                                         Peloderinae;
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                                                                                                      35, Created)
35, Last sequence update)
39, Last annotation updat
me P450 CYP13A5 (EC 1.14.-
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27.0%;
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Pred. No. 2.9e-19;
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RESULT 14
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Q27519;
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PRINTS; PR00385; P450;
PROSITE; PS00086; CYTOCHROME_P450;
  30-MAY-2000
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BINDING 4
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Pfam; PF00067; p450; 1.
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FUNCTION: CYTOCHROMES P450 ARE A GROUP OF HEME-THIOLATE
MONOOXYGENASES. THEY OXIDIZE A VARIETY OF STRUCTURALLY UNRELATED
COMPOUNDS, INCLUDING STEROIDS, FATTY ACIDS, AND XENOBIOTICS.
SIMILARITY: BELONGS TO THE CYTOCHROME P450 FAMILY.
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464 464 HEME (BY SIMILARITY).
20 AA; 59524 MW; 0B7B19E25B7ADF3B CRC64;
                                                                                                          STANDARD;
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InterPro; IPR001128; Cytochrome_P450.
Pfam; PF00067; p450; 1.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   the European Bioinformatics Institute. There are no restrictions use by non-profit institutions as long as its content is in modified and this statement is not removed. Usage by and for commodified and this statement is not removed.
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-I- FUNCTION: CYTOCHROMES P450 ARE A GROUP OF HEME-THIOLATE
MONOOXYGENASES. THEY OXIDIZE A VARIETY OF STRUCTURALLY UNREL
COMPOUNDS, INCLUDING STEROIDS, FATTY ACIDS, AND XENOBIOTICS
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Eukaryota; Metazoa; Nem
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CYP13A7 OR T10B9.10
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PROSITE; PS00086; CYTOCHROME_P450; 1.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        entities requires a
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Gardner A.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Rhabditidae; Peloderinae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              SEQUENCE FROM N.A.
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                                                                                                                                               WVLK-HSNLSTEQILDLILSLLFAGHETSSVAIALAIFFLQACPKAVEELREEHLEIARA
                                                                                                                                                                                                                                                                                                                                                                                                                                                               GKSGWPFLG-----ETIGYLKPYTATTLGDFMQQHVSKYGKIYRSNLFGEPTIVSAD
ELAKLEMAVFIHHLVLKFNWE
                              VDTWSLHHDPKVWGDDVNEFKPERWE---
                                                                                      DRECPDPEVTFDQLSKLKYLECVVKEALRLYPLASLVHNRKCLKTTNVLGMEIEAGTNIN
                                                                                                                  KKELGESELNWDDYKKMDFTQCVINETLRLGNVVRFLH-RKALKDVRYKGYDIPSGWKVL
                                                                                                                                                                                                                                    TILKFIERKMEERKLDIKEEDQE---EEEVKTEDEAEM----SKSDHVRKQRTDDDLLG
                                                                                                                                                                                                                                                                 M----GQEKSLMFRNPMLDKVKTIFKEGRNNVFMISGIFPFVGIALRNIFAKFPSLQMAT
                                                                                                                                                                                                                                                                                              MSMDPGEEET-----EQLKKEYVTFMKG-----VVSAPLNLPGTAYHK-----ALQSRA 236
                                                                                                                                                                                                                                                                                                                           SLRKIMGTVEESVTELVRSLEKASAEGKTLDMLEYYQE------FTMDIIGKMA
                                                                                                                                                                                                                                                                                                                                                        RLRTI------LLKDVER-----HTLFVLDSWQQNSIFSAQDEAKKFTFNLMAKHI 192
                                                                                                                                                                                                                                                                                                                                                                                   P---EFVHEVFVKQFDNFYGRKLTAIQGDPNKNKRVPLVAAQGHRWKRLRTLASPTFSNK 139
                                                                                                                                                                                                                                                                                                                                                                                                                  AGLNRFILQNEGRLFECSYPRSIGGILG-----
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                                                         PVISAVHLDNSRY-DOPNLENPWRWQQQNNGASSSGSGSFSTWGNNYMPFGGGPRLCAGS
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               518 AA;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        license agreement (See http://www.isb-sib.ch/announce/
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Pred. No. 2.
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                              SGDELFFAKG-GYLPFGMGPRICIGM
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RA Herneiser S., Hempel S., Feldpausch M., Lamberth S., Van den Daele H.,
RA De Keyser A., Buysshaert C., Gielen J., Villarroel R., De Clercq R.,
RA Van Montagu M., Rogers J., Cronin A., Quail M., Bray-Allen S.,
RA Clark L., Doggett J., Hall S., Kay M., Lennard N., McLay K., Mayes R.,
RA Clark L., Doggett J., Hall S., Kay M., Lennard N., McLay K., Mayes R.,
RA Borkova D., Bloecker H., Scharfe M., Grimm M., Loehnert T.-H.,
RA Borkova D., Bloecker H., Scharfe M., Meller-Auer S.,
RA Borkova D., Bloecker H., Scharfe M., Mueller-Auer S.,
RA Borkova D., Argirion A., Vitale D., Liguori R., Piravandi E.,
RA Mossenet O., Quigley F., Clabauld G., Muendlein A., Felber R.,
RA Massenet O., Quigley F., Clabauld G., Muendlein A., Felber R.,
RA Chefdor F., Cooke R., Berger C., Monfort A., Casacuberta E.,
RA Chefdor F., Cooke R., Berger C., Monfort A., Casacuberta E.,
RA Gibbons T., Weber N., Vandenbol M., Bargues M., Terol J., Torres A.,
RA Frishman D., Haase D., Lemcke K., Mewes H.-W., Stocker S.,
RA Frishman D., Haase D., Lemcke K., Mewes H.-W., Stocker S.,
RA Parnell L., Dedhia N., Gnoj L., Schutz K., Huang E., Spiegel L.,
RA Sekhon M., Murray J., Sheet P., Cordes M., Abu-Threideh J.,
RA Stoneking T., Kalicki J., Graves T., Harmon G., Edwards J.,
RA Minx P., Bentley D., Fulton B., Miller N., Greco T., Kemp K.,
RA Minx P., Bentley D., Fulton B., Miller N., Greco T., Kemp K.,
RA Minx P., Spieth J., Ryan E., Andrews S., Geisel C., Layman D.,
RA Melson J., Spieth J., Ryan E., Andrews S., Geisel C., Layman C.,
RA Melson J., Spieth J., Ryan E., Andrews S., Geisel C., Layman C.,
RA Melson J., Spieth J., Schwer S., Borne K., Cotton M., Joshu C.,
RA Melson J., Spieth J., Schwer M., Matero A., Shah R.,
Na Shaby I.K., O'Shaudhnessy A., Rodriduez M., Hoffman J., Shah R.,
Swaby I.K., O'Shaughnessy A., Rodriguez M., Hoffman Granat S., Shohdy N., Hasegawa A., Hameed A., Lodhi Chen E., Marra M., Martienssen R., McCombie W.R.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Langham S.-A., McCullagh B., Bilham L., Robben J.,
Van der Schueren J., Grymonprez B., Chuang Y.-J., Vandenbussche
Braeken M., Weltjens I., Voet M., Bastiaens I., Aert R., Defoor
Weitzenegger T., Bothe G., Ramsperger U., Hilbert H., Braun M.,
Holzer E., Brandt A., Peters S., van Staveren M., Dirkse W.,
Mooijman P., Klein Lankhorst R., Rose M., Hauf J., Koetter P.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       MEDLINE=20083488; PubMed=10617198;
Mayer K.F.X., Schueller C., Wambutt R., Murphy G., Volckaert
Pohl T., Duesterhoeft A., Stiekema W., Entian K.-D., Terryn
Harris B., Ansorge W., Brandt P., Grivell L.A., Rieger M.,
Weichselgartner M., de Simone V., Obermaier B., Mache R., Mus
Weichselgartner M., de Simone V., Obermaier B., Mache R., Mus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    "Cytochrome P450 superfamily in Arabidopsis thaliana: isolation cDNAs, differential expression, and RFLP mapping of multiple cytochromes P450.";
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MEDLINE=98281573;
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16-OCT-2001 (Rel. 40, Created)
16-OCT-2001 (Rel. 40, Last ser
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Vos P., Hohelsel J., Zimmermann W., Wedler H., Ridley P.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Weichselgartner M., de
Kreis M., Delseny M.,
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Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;

Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; Rosid;

eurosids II; Brassicales; Brassicaceae; Arabidopsis.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Columbia; TISSUE=Seedling;
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                                     Lodhi M., Johnson A.,
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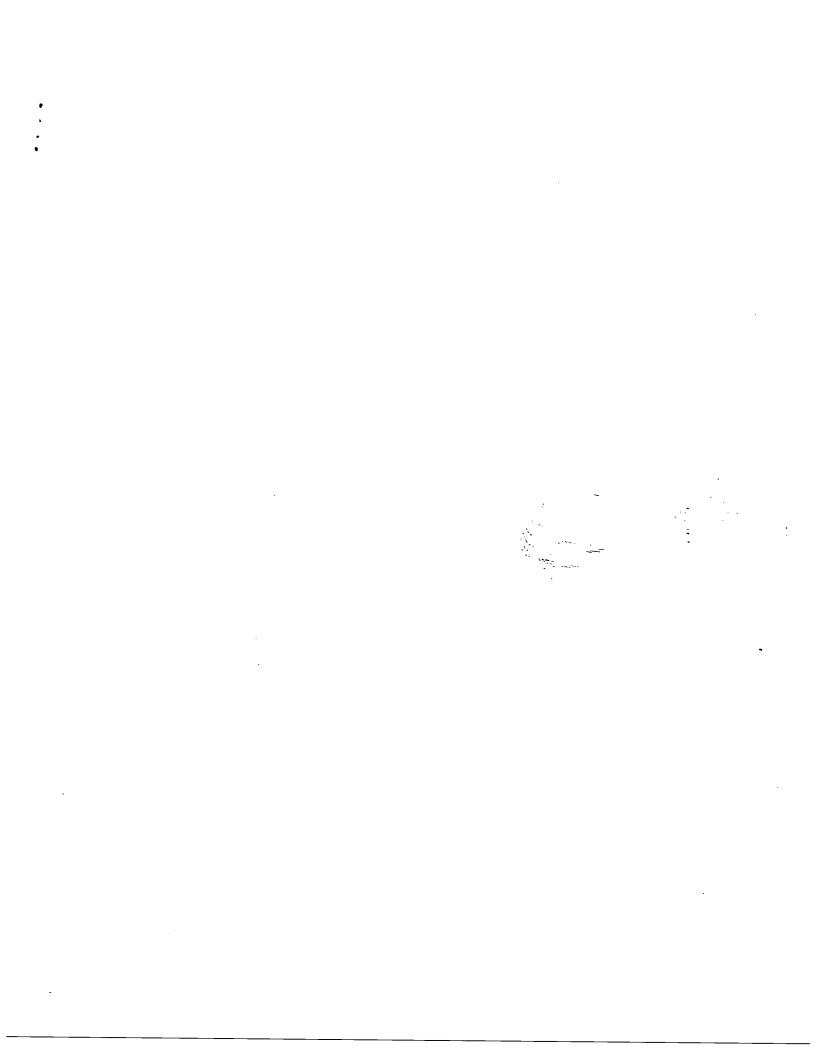
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EMBL; AL035601; CAB38210.1; -.
InterPro; IPR001128; Cytochrome_P450.
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                                                                                                                                                                                                                                                                 164 ---NESNDFTHIELEPLLSDLTFNNIVRMVTGKRYYGDDVNNKEEAELFKK------
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Nature 402:769-777(1999)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 "Sequence and analysis of chromosome 4 of the plant Arabidopsis thaliana.";
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                                                                          L-HRKALKDVRYKGYDIPSGWKVLPVISAVHLDNSRYDQPNLFNPWRWQQQNNGASSSGS
                         GSFSTWGNNY-----MPFGGGPRLCAGSELAKLEMAVFIHHLVLKFNWELAEDDQ
                                                   LIPRSPTDDMKIGGYDVPRDTIVMVNAWAIHRDPEIWEEPEKENPDRY---NDGC----
                                                                                                    ANLLRNPEVLEKARSE-----IDEKIGKDRLIDESDIAVLPYLQNVVSETFRLFPVAPF
                                                                                                                              FFLQACPKAVEELREEHLEIARAKKELGESEL-NWDDYKKMDFTQCVINETLRLGNVVRF
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SEQUENCE FROM N.A.
Chen H.,
                                                                                                                                   Cheuk R., Chen H., Kim C.J., Koesema E., Meyers M.C., Banh J., Bowser L., Carninci P., Dale J.M., Goldsmith A.D., Hayashizaki Y., Ishida J., Jiang P.X., Jones T., Kamiya A., Karlin Neumann G., Kawai J., Lam B., Lee J.M., Lin J., Liu S.X., Miranda M., Narusaka Nguyen M., Onodera C.S., Palm C.J., Pham P.K., Quach H.L., Sakurai Satou M., Seki M., Southwick A., Tang C.C., Toriumi M., Yamada K., Yamamura Y., Yu G., Yu S., Shinozaki K., Davis R.W., Theologis A.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Arabidopsis thaliana (Mouse-ear cress).

Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;

Spermatophyta; Magnoliophyta; eddicotyledons; core eudicots; Rosidae;

eurosids II; Brassicales; Brassicaceae; Arabidopsis.
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RESULT
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O9LKH7; PRELIMINARY;
O9LKH7;
O1LCT-2000 (TrEMBLrel. 1
01-OCT-2000 (TrEMBLrel. 1
01-JUN-2002 (TrEMBLrel. 2

15, 15, 21,

Created)
Last sequence update)
Last annotation updat

update)

PRELIMINARY;

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Cytochrome P450.

CYP90A2.

Vigna radiata.

Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; Roside eurosids I; Fabales; Fabaceae; Papillonoideae; Phaseoleae; Vigna.

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EMBL; AL132979; CAB62435.1; -.
EMBL; AR412114; AAL06567.1; -.
EMBL; AR90266; AAL09927.1; -.
EMBL; AV90266; AAL09927.1; -.
InterPro; IPR001128; Cytochrome_P450.
PFAm; PF00067; P450; 1.
PFANTS; PR00385; P450; 1.
PROSITE; PS00086; CYTOCHROME_P450; UNKNOWN_1.
Heme: Monooxygenase; Oxidoreductase.
SEQUENCE 513 AA; 58867 MW; B1639BDD9A5D7C93
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Seki M., Sc
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Kawai J., Lam B
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                                                               QPNLFNPWRWQQQNNGASSSGSGSFSTWGNNYMPFGGGPRLCAGSELAKLEMAVFIHHLV
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                                                                                                                YKKMDFTQCVINETLRLGNVVRFLHRKALKDVRVKGYDIPSGWKVLPVISAVHLDNSRYD
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                                                QPNLFNPWRWQQQNNGASSSGSGSFSTWGNNYMPFGGGPRLCAGSELAKLEMAVFIHHLV
                                                                                                    YKKMDFTQCVINETLRLGNVVRFLHRKALKDVRYKGYDIPSGWKVLPVISAVHLDNSRYD
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Yu G., Yu
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                                                                                                                                             Q9FX29 PRELIMINARY; PRT; 512 AA.
Q9FX29;
Q1-MAR-2001 (TIEMBLrel. 16, Created)
Q1-MAR-2001 (TIEMBLrel. 16, Last sequence update)
Q1-MAR-2002 (TIEMBLrel. 20, Last annotation update)
Steroid 22-alpha-hydroxylase, putative.
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; Roslid eurosids II; Brassicales; Brassicaceae; Arabidopsis.

[1]
                                                                                                     Arabidopsis thaliana (Mouse-ear cress).
                                                                                                                                   T9L24.44.
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InterPro; IPR001128; Cytochrome_P450.
Pfam; PF00067; P450; 1.
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PROSITE; PS00086; CYTOCHROME_P450;
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NCE 474 AA; 54037 MW; A2542A809C5BAC6D CRC64;
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Pred. No. 3e-60;
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Best Local S
Matches 181
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-- SIMILARITY: BELONGS TO THE CYTOCHROME P450 FAMILY.
EMBL; AC012396; AAG30983.1; --
InterPro; IPRO01128; Cytochrome_P450.
PFam; PF00067; p450; 1.
PRNNTS; PR00085; P450.
PROSITE; PR00085; P450.
PROSITE; PR00085; P450.
PROSITE; PR00085; P450.
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SEQUENCE 512 AA; !
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                              GGTRFCPGAELARLQIALFLHYFITTYKWTQLKEDRISFFPSARLVNGFKIQLNR
                                              GGPRLCAGSELAKLEMAVFIHHLVLKFNWELAEDDQPFAFPFVDFPNGLPIRVSR
                                                                               GCFVVPfLSAVHLDESYYKESLSFNPWRWLDPETQQKRNWRTSP-----FYCPFG
                                                                                                GWKVLPVISAVHLDNSRYDQPNLFNPWRW-----QQQNNGASSSGSGSFSTWGNNYMPFG
                                                                                                                                   -----DRLAGGMLTWQDYKTNDFTQCVIDETLRLGGIAIWLMREAKEDVSYQDYVIPK
                                                                                                                                                LEIARAKKELGESELNWDDYKKMDFTQCVINETLRLGNVVRFLHRKALKDVRYKGYDIPS
                                                                                                                                                                                                    LFVLDSWQQNSIFSAQDEAKKFTFNLMAKHIMSMDPGEEETEQLKKEYVTFMKGVVSAPL
                                                                                                                                                                                                                                                                                                                                            AGNGVLGRLLEEESLPNESMADFIINLLFAGNETTSKTMLFAVYFLTHCPKAMTQLLEEH
                                                                                                                                                                                                                                             DLPGFTYNKAMKARKEIIRKINKTIEKRLQNKAASD-----
                                                                                                                                                                                                                                                                  NLPGTAYHKALQSRATILKFIERKMEERKLDIKEEDQEEEEVKTEDEAEMSKSDHVRKQR
                                                                                                                                                                                                                                                                                           LQTLSNFKDGEVVLLQDICRKVAIHLMVNQLLGVS-SESEVDEMSQLFSDFVDGCLSVPI
                                                                                                                                                                                                                                                                                                                                                                                                FVEKQIKKFVSLLCSVLLLILKRPDNSGFNEIRYGRIFSCSLFGKWAVVSADPDFNRFIM
                                                                                                                                                                                                                                                                                                                                                                                                                        FMQQHVSK------YGKIYRSNLFGEPTIVSADAGLNRFIL
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Pred. No. 4.2e-54;
5; Mismatches 173;
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RESULT
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ID Q9
ID Q9
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DT 011
DT 011
DT 011
DT 02
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01-DEC-2001
01-JUN-2002
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Q94IA6;
                                                                                                                                     Arabidopsis thaliana (Mouse-ear cress).

Eukaryota; Viridiplantae; Streptophyta; Embryophyta;
Spermatophyta; Magnollophyta; eudicotyledons; core eueurosids II; Brassicales; Brassicaceae; Arabidopsis.
SEQUENCE FROM N.A
                                                          NCBI_TaxID=3702; [1]
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(TrEMBLrel.
(TrEMBLrel.
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RESULT 6
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Best Local S
Matches 176
Toriumi M., Foker J.R.;
          SEQUENCE FROM N.A.

Chao Q., Brooks S., Buehler E., Johnson-Hopson C., Khan S., Kim C., Chao Q., Brooks S., Buehler E., Johnson-Hopson C., Choi E., Conn L., Shinn P., Altafi H., Bei Q., Chin C., Chiou J., Choi E., Conn L., Shinn P., Gonzales A., Hansen N., Howng B., Koo T., Lam B., Iee J., Lonz C., Li J., Liu A., Liu K., Liu S., Mukharsky N., Nguyen M., Palm C., Pham P., Sakano H., Schwartz J., Southwick A., Thaveri A., Poriumi M., Vaysberg M., Yu G., Federspiel N.A., Theologis A.,
                                                                                                                                                                                  Arabidopsis thaliana (Mouse ear cress).

Bukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;

Spermatophyta; Magnollophyta; eudicotyledons; core eudicots; Rosidae;

eurosids II; Brassicales; Brassicaceae; Arabidopsis.

NCBI_TaxID-3702;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             "P450 gene repressed by brassinosteroid.";
Submitted (JUI-2001) to the EMBL/GenBank/DDBJ databases.
-!-SIMILARITY: BELONGS TO THE CYTOCHROME P450 FAMILY.
EMBL; AB066286; BAB62109.1; -.
InterPro; IPR001128; Cytochrome_P450.
InterPro; IPR000504; RNA_rec_mot.
Pfam; PF00067; p450; 1.
PROSITE; PS00086; CYTOCHROME_P450; UNKNOWN_1.
PROSITE; PS00030; RRM_RNP_1; UNKNOWN_1.
                                                                                                                                                                                                                                                                                                             Q9LN73;
01-OCT-2000 (TrEMBLrel. 15,
01-OCT-2000 (TrEMBLrel. 15,
01-JUN-2002 (TrEMBLrel. 21,
                                                                                                                                                                                                                                                                                                                                                                                                  Q9LN73
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Shimada Y.;
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NCE 491 AA;
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PS00030; RRM_RNP_1; UNKNOWN_1.
nooxygenase; Oxidoreductase.
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Last sequence update)
Last annotation updat
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Matches 181
                                                                                SEQUENCE FROM
                                                                                                                    NCBI_TaxID=3702;
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Submitted (JAN-2001) to the EMBL/GenBank/DDBJ databases.
-- SIMILARITY: BELONGS TO THE CYTOCHROME P450 FAMILY.
EMBL; AC025417; AAF88087.1; --
InterPro; IPR001128; Cytochrome_P450.
Pfam; PF00067; p450; 2.
Pfam; PF00067; p450; 2.
PRINTS; PR000385; P450.
PROSITE; PS00086; CYTOCHROME_P450; UNKNOWN_1.
Heme: Monooxygenase; Oxidoreductase.
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YRWEEIKGGNITRTPGLQFPNGYHVKLHK
                                                                                                                NLFNPWRWQQQNNGASSSGSGSFSTWGNNYMPFGGGPRLCAGSELAKLEMAVFIHHLVLK 482
                                                                                                                                                                                CVINETLRLGNVVRFLHRKALKDVRYK------GYDIPSGWKVLPVISAVHLDNSRYDQP
                                                                                                                                                                                                                                                                                                   LFAGHETSSVAIALAIFFLQACPKAVEELREEHLEIARAKKELGESELNWDDYKKMDFTQ
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                                             FWELAEDDOPFAFPFVDFPNGLPIRVSR
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                                                                                          LVFNPSRWE---
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RCE 478 AA; 55058 MW; F67A
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                                                                                          -GSKVTNASKHFMAFGGGMRFCVGTDFTKLQMAAFLHSLVTK
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Pred. No. 5.6e-51;
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O9LY89;
O1-OCT-2000 (TrEMBLrel. 15, C
O1-OCT-2000 (TrEMBLrel. 15, L
O1-MAR-2002 (TrEMBLrel. 20, L
Hypothetical 43.9 kDa protein
F18022_190.
Bevan M., Murphy G., I
Rudd S., Lemcke K., Ma
Submitted (APR-2000) t
[2]
                                                                                                           Arabidopsis thaliana (Mouse-ear cress).

Eukaryota; Viridiplantae; Streptophyta; Embryophyta;
Spermatophyta; Magnoliophyta; eudicotyledons; core eu
eurosids II; Brassicales; Brassicaceae; Arabidopsis.
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Last sequence update)
               EMBL/GenBank/DDBJ databases
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Rosidae;

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RESULT Q94 IVE AC Q5 DT Q91 DT
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Best Local S
Matches 159
                                          STRAIN-CV. NIPPONBARE
Sasaki T., Matsumoto
                                                                                                                                                                                                                                                                          Oryza sativa (Rice).

Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Trach Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; Ehrhartoideae; Oryzeae; Oryza.
                                                                                                                                                                                                                                                                                                                                                                                094IW5 PRELIMINARY; PRT; 490 AA. 094IW5; PTELIMINARY; PRT; 490 AA. 01-DEC-2001 (TIEMBLIE1. 19, Created) 01-DEC-2001 (TIEMBLIE1. 19, Last sequence up 01-JUN-2002 (TIEMBLIE1. 21, Last annotation Cytochrome P450-like protein. P0419B01.5.
                                                                                                                                                                                                                 SEQUENCE FROM N.A.
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Submitted (APR-2000) to the EMBL/GenBank/DDBJ databases.
-!- SIMILARITY: BELONGS TO THE CYTOCHROME P450 FAMILY.
EMBL; AL163817; CAB87779.1; -.
InterPro; IPR001128; Cytochrome_P450.
Pfam; PF00067; p450; 1.
PROSITE; PS00086; CYTOCHROME_P450; UNKNOWN_1.
Heme; Hypothetical protein; Monooxygenase; Oxidoreductase.
SEQUENCE 382 AA; 43889 MW; 18C5685AB73B4E30 CRC64;
                           InterPro;
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  PF00067;
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IPR001128; Cytochrome_P450 0067; p450; 1.
                                                                                                                                                        NIPPONBARE;
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34.2%; Pred. No. 1.3e-50;
tive 87; Mismatches 127
                                                                                                                                 Yamamoto K.; (GA3) genomic
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Heme; Monooxygenase; Oxidoreductase.
SEQUENCE 490 AA; 54824 MW; 9EC2853BBAFBB8
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          WELAEDDQPFAFPFVDFPNGLPIRVS
W-VAEEDHIVNFPTVRLKRGMPIRVT
                                   FNPWRWQQQNNGASSSGSGSFSTWGNNYMPFGGGPRLCAGSELAKLEMAVFIHHLYLKFN
                                                                           SFTQHVITETLRLGNIIGGIMRKAVRDVEVKGHLIPKGWCVFVYFRSVHLDDTLYDEPYK
                                                                                                                    MIDLMIPAEDSVPVLITLAVKFLSECPLALHQLEEENIQLKRRKTDMGET-LQWTDYMSL
                                                                                       -----LDIKEEDQEEEEVKTEDEAEMSKSDHVRKQRTDDDLLGWVLKHSNLSTEQILDL
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                                                                                                                               SPPRDAIDVLIGDGSDE-----
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                                                                                                                                                                                                                                            HGLVGAFFKSSHLKSQLTADMRRRLSPALSSFPDSSLLHVQHLAKSVVFEILVRGLIGLE
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                                                                                                                                                                                                                                                                                   AVFRSHLFGSATVVTADAEVSRFVLQSDARAFVPWYPRSLTELMGKSSILLINGALQRRV
                                                                                                                                                                                                                                                                                                LLRRRRRGAGSGKGDAAAAARLPPGSFGWPVVGETLEFVSCAYSPRPEAFVDKRRKLHGS
                                                                                                                                                                                                                                                                                                                                                                                     Similarity
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                                                                                                                                                                                                                                                                                                                                                                                                                54824 MW;
                                                                                                                                                                                                                                                                                                                                                                                 30.3%;
                                                                                                                                                                                                                                                                                                                                                                         106;
                                                                                                                                                                                                                                                                                                                                                                                 Score 813.5; DB Pred. No. 2.4e-50
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484
                  510
                                                                                                                                                                                                                                                                                                                                                                       Mismatches
                                                                                                                                                                                                                                                                                                                                                                                           DB 10;
                                                                                                                                                                                                                                                                                                                                                                       156;
                                                                                                                                                                                                                                                                                                                                                                                                               CRC64;
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                                                                                                                                                            ---LTDELISDN
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RESULT
Q9LIC5
       "Structural analysis of A
"Structural analysis of the
Sequence features of the
TAC and BAC clones.",
DNA Res. 7.217-221(2000)
                                                                                                                                                          Cytochrome P450-like protein.

Cytochrome P450-like protein.

Arabidopsis thaliana (Mouse-ear cress).

Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheop Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; eurosids II; Brassicales; Brassicaceae; Arabidopsis.
                                                                                                                                                                                                                       Q9LIC5;
01-OCT-2000 (TrEMBLrel. 15,
01-OCT-2000 (TrEMBLrel. 15,
01-JUN-2002 (TrEMBLrel. 21,
                                                             STRAIN=COLUMBIA;
MEDLINE=20363099;
                                                                                                       Kaneko T., Kato T.,
Submitted (MAR-2000)
                                                                                                                           SEQUENCE FROM N.A.
STRAIN-COLUMBIA;
                                                                                   SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                     Q9LIC5
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Res. 7:217-2
SIMILARITY:
                                                                                                                                                                                                                                                                  PRELIMINARY;
BELONGS
                                                            PubMed=10907853;
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                             Arabidopsis
e regions of
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                                                                                                     Asamizu E., T
DDBJ databases
                            chromosome
5 bp covered
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                                                                                                                                                                                      Tracheophyta;
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                            ninety
                                                                                                              s.;
                                                                                                                                                                             Rosidae;
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THE

CYTOCHROME P450 FAMILY

7;

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RESULT 10
Q8WORD
ID Q8WORD
AC Q8WORD
AC Q8WORD
DT 01-MA
DT 01-JU
DE SB32H
GN SB32H
GN SB32H
GN SB32H
GN SB32H
GN SB32H
GN SB3E
GN SEGUE
RN [1]
RP SEGUE
RC STRAI
RN [2]
RN SEGUE
RA SUBMI
RN SEGUE
RC STRAI
RN [2]
RN SEGUE
RC STRAI
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Best Local Sin
Matches 163;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 R InterPro; IPR001128; Cytochrome_P450.
R InterPro; IPR0001504; RNA_rec_mot.
R Pfam; PF00067; p450; 1.
R PRINTS; PR00385; P450,
R PRINTS; PS00086; CYTOCHROME_P450; UNKNOWN_1.
R PROSITE; PS00086; CYTOCHROME_P450; UNKNOWN_1.
RPROSITE; PS00030; RRM_RNP_1; UNKNOWN_1.
Heme; Monooxygenase; Oxidoreductase.
SEQUENCE 464 AA; 52864 MW; A65E094665PF100D
                                                                                                                                                                                                                                                                                                                           Q8W0R4;

Q1-MAR-2002 (TrEMBLrel. 20, Created)

Q1-MAR-2002 (TrEMBLrel. 20, Last sequer

Q1-JUN-2002 (TrEMBLrel. 21, Last annot;

Q1-tastive cytochrome P450-like protein.
             STRAIN-CV. BTX623;
Llaca V., Young S., Kovchok
Submitted (JAN-2002) to the
EMBL; AF466201; AAL/3372.1;
                                                                                                                                              SEQUENCE FROM N.A. STRAIN-CV. BTX623; Park Y.-J., Ramakr
                                                                                                                                                                                                                                   SB32H17.4.
Sorghum bicolor (Sorghum) (Sorghum vulgare).
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; PACC clade;
Panicoldeae; Andropogoneae; Sorghum.
                                                                                                                                                                                                                                                                                                                                                                                                                                            Q8W0R4
                                                                                                                                Submitted (JAN-2002)
 InterPro;
                                                                                             SEQUENCE FROM N.A.
                                                                                                                                                                                                                               NCBI_TaxID=4558;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         437
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                PLNLPGTAYHKALQSRATILKFIERKMEERKLDIKEEDQEEEEVKTEDEAEM---SKSDH
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    FLSESMDLWSEDQPVLLQDVSKTVAFKYLAKALISVEKG-EDLEELKREFENFISGLMSL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         HTLFVLDSWQQNSIFSAQDEAKKFTFNLMAKHIMSMDPGEEETEQLKKEYVTFMKGVVSA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               VLQSDSTAFVPFYPKTVRELMGKSSILLINGSLHRRFHGLVGSFLKSPLLKAQIVRDMHK
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        PHGSLGWPVIGETIEFVSSAYSDRPESFMDKRRLMYGRVFKSHIFGTATIVSTDAEVNRA 111
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              PPGKSGWPFLGETIGYLKPYTATTLGDFMQQHVSKYGKIYRSNLFGEPTIVSADAGLNRF
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ILQNEGRLFECSYPRSIGGILGKWSMLVLVGDMHRDMRSISLNFLSHARLRTILLKDVER
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 IPR001128;
                                                                                                                                Ramakrishna
JAN-2002) to
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 Cytochrome_P450
                                                                                                                                  W.,
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                                 S., Messing J.;
EMBL/GenBank/DDBJ
                                                                                                                                                                                                                                                                                                                                                            Last sequence update)
Last annotation update)
                                                                                                                                SanMiguel P., Embe EMBL/GenBank/DDBJ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Score 789;
Pred. No. 1
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.3e-48;
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                                                                                                                                                  Emberton J.,
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Best Local Sim
Matches 170;
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Q9FMA5;
01-MAR-2001 (TTEMBLTel. 1
01-MAR-2001 (TTEMBLTEL 1
01-MAR-2002 (TTEMBLTEL 2
SEQUENCE FROM N.A STRAIN-COLUMBIA; MEDLINE-21295570;
                                                                                                                                                                           Sato S., K
Tabata S.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Pfam; PF00067; p450; 1.
PROSITE; PS00086; CYTOCHROME_P450; UNKNOWN_1
SEQUENCE 481 AA; 54984 MW; 6145CFFFCOFP7.
                                                                   DNA
[2]
                                                                                     "Structural analysis of Arabidopsis thaliana chrosequence features of the regions of 1,456,315 bp physically assigned Pl and TAC clones."; DNA Res. 5:41-54(1998).
                                                                                                                                                                                                                                                                                                                              Arabidopsis thaliana (Mouse-ear cress).
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; Rosid;
eurosids II; Brassicales; Brassicaceae; Arabidopsis.
                                                                                                                                                                                                                                                                                                                                                                                                                                        Cytochrome
                                                                                                                                                                                                                      STRAIN-COLUMBIA;
MEDLINE-98290546;
                                                                                                                                                                                                                                                                 SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                          NCBI_TaxID=3702;
                                                                                                                                                                                                                                                                                                                                                                                                                      BR60XI.
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., Kotani H., Nakamura
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Q944V4;

Q944V4;

Q944V4;

Q1-DEC-2001 (TrEMBLrel. 19, Created)

Q1-DEC-2001 (TrEMBLrel. 19, Last sequence update)

Q1-DEC-2001 (TrEMBLrel. 21, Last annotation update)

Q1-JUN-2002 (TrEMBLrel. 21, Last annotation update)

Q1-JUN-2002 (TrEMBLrel. 21, Last annotation update)

Q2-2003 Arabidopsis thaliana (Mouse-ear cress).

Q2-2004 Arabidopsis thaliana (Mouse-ear cress).

Q3-2004 Embryophyta; Tra

Q45 AA.

Q46 AA.

Q46 AA.

Q47 AA.

Q46 AA.

Q47 AB.

Q46 AA.

Q47 AB.

Q48 AB.

Q48 AB.

Q48 AB.

Q48 AB.

Q49 AB.

Q48 AB.

Q49 AB.

Q49 AB.

Q49 AB.

Q40 AB.

Q4
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"I SIMILARITY: BELONGS TO THE CYTOCHROME P450 FAMILY. EMBL; AB009048; BAB08653.1; -.
EMBL; AB095868; BAB60858.1; -.
EMBL; AB035868; BAB60858.1; -.
InterPro; IPR001128; Cytochrome_P450.
Pfam; PF00067; P450; 1
PRINTS; PS00086; CYTOCHROME_P450; UNKNOWN_1.
                                 Cheuk R., Chen H.,
                                                        SEQUENCE FROM N.A.
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Kim C.J., Koesema E., Meyers M.C.,
if P., Dale J.M., Goldsmith A.D., Ha
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32.3%; Pre
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Pred. No. 4.3e-44;
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Best Local S
Matches 163
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Kim C.J., Chen H., Cheuk R., Meyers M.C., Banh J., Bowser L., Carninci P., Chang E., Dale J.M., Goldsmith A.D., Hayashizaki Y., Ishida J., Jones T., Kamiya A., Karlin-Neumann G., Kawai J., Lam B., Lee J.M., Lin J., Miranda M., Narusaka M., Nguyen M., Onodera C.S., Palm C.J., Quach H.L., Sakurai T., Satou M., Seki M., Southwick A., Tang C.C., Toriumi M., Wu H.C., Yanada K., Yamamura Y., Yu G., Yu S. Shinozaki K., Davis R.W., Theologis A., Ecker J.R.; "Arabidopsis ORF clones."; Submitted (NOV-2001) to the EMBL/GenBank/DDBJ databases.

-I- SIMILARITY: BELONGS TO THE CYTOCHROME P450 FAMILY.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           InterPro; IPR001128; Cytochrome_P450.
Pfam; PF00067; p450; 1.
PROSITE; PS00086; CYTOCHROME_P450; UNKNOWN_1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Ishida J., Jiang P.X., Jones T., Kamiya A., Karlin-Neumann G., Kawai J., Lam B., Lee J.M., Lin J., Liu S.X., Miranda M., Narusaka Nguyen M., Onodera C.S., Palm C.J., Pham P.K., Quach H.L., Sakurai Yamadu M., Seki M., Southwick A., Tang C.C., Torlumi M., Yamada K., Yamadaura Y., Yu G., Yu S., Shinozaki K., Davis R.W., Theologis A.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        EMBL; AY052655; AAK96559.1; -. EMBL; AY063728; AAL36078.1; -.
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hes 163;
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                                       RWEENGEDKLMVFPRVSAPKGYHLKCS
                                                                  NWELAEDDQPFAFPFVDFPNGLPIRVS
                                                                                                            MKFTRAVIFETSRLATIVNGVLRKTTHDLELNGYLIPKGWRIYVYTREINYDTSLYEDPM
                                                                                                                                                                          MDFTQCVINETLRLGNVVRFLHRKALKDVRYKGYDIPSGWKVLPVISAVHLDNSRYDQPN 423
                                                                                                                                                                                                       LVGDMHRDMRSISLNFLSHARLRTILLKDVERHTLFVLDSWQQNSIFSAQDEAKKFTFNL
                                                                                                                                                                                                                                                                                                                                                  MAKHIMSMDPGEEETEQLKKEYYTFMKGVVSAPLNLPGTAYHKALQSRATILKFIERKME
                                                                                                                                                                                                                                                                                                                                                                                VHGPSHRLMRGSLLSLISPTMMKDHLLPKIDDFMRNYLCGWDDLETVDIQEKTKHMAF-L
                                                                                                IFNPWRWMEKSLESKS---
                                                                                                                                                                                                                                                                                  ERKLDIKEEDQEEEEVKTEDEAEMSKSDHVRKQRTDDDLLGWVLKHSN----LSTEQILD
                                                                                                                                                                                                                                                                                                                       SSLLQIAETLKKPEVEEYRTEFFKLVVGTLSVPIDIPGTNYRSGVQARNNIDRLLTELMQ
                                                                                                                                                                                                                                                                                                                                                                                                                                       MQQHVSKYGKIYRSNLFGEPTIVSADAGLNRFILQNEGRLFECSYPRSIGGILGKWSMLV
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Conservative
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32.1%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         94;
                                                                                             ---YFLLFGGGVRLCPGKELGISEVSSFLHYFVTKY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Pred. No. 4.3e
4; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Score 712; DB 10;
Pred. No. 4.3e-43;
                                                                                                                                                                                                                                                                  -----DMLGYLMKKEDNRYLLTDKEIRD
                                       463
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Best Local Sim
Matches 163;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   TAC and BAC clones.";

DNA Res. 7:217-221(2000).

-1- SIMILARITY: BELONGS TO THE CYTOCHROME P450:
EMBL; AP002060; BAB02270.1; -.

InterPro; IPR001128; Cytochrome_P450.
Pfam; PP00007; p450; D450.
PRINTS; PR00385; P450.
PRINTS; PR00385; P450.
PROSITE; PS00086; CYTOCHROME_P450; UNKNOWN_1.

Heme: Monooxygenase; Oxidoreductase.
SEQUENCE 465 AA; 53862 MW; 630A21D0765E0D0D
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Arabidopsis thaliana (Mouse-ear cress).
Arabidopsis thaliana (Mouse-ear cress).
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; Rosidae;
eurosids II; Brassicales; Brassicaceae; Arabidopsis.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Sequence features of TAC and BAC clones.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  STRAIN-COLUMBIA;
Kaneko T., Kato T.,
Submitted (MAY-2000)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        01-OCT-2000 (Tremblrel.
01-OCT-2000 (Tremblrel.
01-MAR-2002 (Tremblrel.
Cytochrome P450.
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437
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                                                                                                                                                                                                                                                                                                                                                                                                  LVGDMHRDMRSISLNFLSHARLRTILLKDVERHTLFVLDSWQQNSIFSAQDEAKKFTFNL 187
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           LLPSLLSLLLFLILL-----KRRNRKTRFNLPPGKSGWPFLGETIGYLKPYTATTLGDF
                         NWELAEDDOPFAFPFVDFPNGLPIRVS
                                                                                                                                                                                                                                                                                                         SSLLQIAETLKKPEVEEYRTEFFKLVVGTLSVPIDIPGTNYRSGFQARNNIDRLLTELMQ
                                                                                                                                                                                                                                                                                                                                     MAKHIMSMDPGEEETEQLKKEYVTFMKGVVSAPLNLPGTAYHKALQSRATILKFIERKME 247
                                                                                                                                                                                                                                                                                                                                                                     VHGPSHRLMRGSLLSLISPTMMKDHLLPKIDDFMRNYLCGWDDLETVDIQEKTKHMAF-L
                                                                                      LFNPWRWQQQNNGASSSGSGSFSTWGNNYMPFGGGPRLCAGSELAKLEMAVFIHHLVLKF
                                                                                                                       MKFTRAVIFETSRLATIVNGVLRKTTHDLELNGYLIPKGWRIYVYTREINYDTSLYEDPM
                                                                                                                                                  MDFTQCVINETLRLGNVVRFLHRKALKDVRYKGYDIPSGWKVLPVISAVHLDNSRYDQPN
                                                                                                                                                                                  QVVTILYSGYETVSTTSMMALKYLHDHPKALEELRREHLAIRERKRP--DEPLTLDDIKS
                                                                                                                                                                                                                                                            ERKLDIKEEDQEEEEVKTEDEAEMSKSDHVRKQRTDDDLLGWVLKHSN----LSTEQILD
                                                                                                                                                                                                                                                                                                                                                                                                                                 MKNQRLRYGSFFKSHILGCPTIVSMDAELNRYILMNESKGLVAGYPQSMLDILGTCNIAA
                                                                                                                                                                                                                                                                                                                                                                                                                                                              MQQHVSKYGKIYRSNLFGEPTIVSADAGLNRFILQNEGRLFECSYPRSIGGILGKWSMLV 127
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32.1%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      of Arabidopsis thaliana chromosome 3. the regions of 4,251,695 bp covered b
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Last sequence
Last anno
                                                        ---YFLLFGGGVRLCPGKELGISEVSSFLHYFVTKY
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Pred. No. 5.1e-43;
3; Mismatches 195;
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                                                                                                                                                                                                                                              -DMLGYLMKKEDNRYLLTDKEIRD
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A Deng J.M., Goldsmith A.D., Lee J.M., Onodera C.S., Quach H.L.,
A Tang C., Toriumi M., Wu H.C., Yamamura Y., Yu G., Bowser L.,
A Carninci P., Chen H., Cheuk R., Hayashizaki Y., Ishida J., Jones T.
A Kamiya A., Karlin-Neumann G., Kawai J., Kim C., Lam B., Lin J.,
A Meyers M.C., Miranda M., Narusaka M., Nguyen M., Palm C.J.,
A Meyers M.C., Miranda M., Narusaka M., Nguyen M., Palm C.J.,
A Meyers M.C., Miranda M., Shinn P., Southwick A., Shinozaki K.
A Sakurai T., Satou M., Seki M., Shinn P., Southwick A., Shinozaki K.
A Davis R.W., Ecker J.R., Theologis A.;
B Davis R.W., Ecker J.R., Theologis A.;
T "Arabidopsis Open Reading Frame (ORF) Clones.";
Submitted (MAR-2002) to the EMBL/GenBank, DDBJ databases.
C -!- SIMILARITY: BELONGS TO THE CYTOCHROME P450 FAMILY.
REMBL; AY050980; AAK93657.1; -.
REMBL; AY050980; AAK93657.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                  Matches
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Q949P1;
01-DEC-2001
01-DEC-2001
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        SEQUENCE FROM N.A.

Yamada K., Liu S.X., Pham P.K., Banh J., Banno F., Dale J.M.,

Goldsmith A.D., Jiang P.X., Lee J.M., Onodera C.S., Quach H.L.,

Tang C., Toriumi M., Yamamura Y., Yu G., Yu S., Bowser L.,

Tang C., Toriumi M., Yamamura Y., Yu G., Yu S., Bowser L.,

Carninci P., Chen H., Cheuk R., Hayashizaki Y., Ishida J., Jones

Kamiya A., Karlin-Neumann G., Kawai J., Kim C., Koesema E., Lam B

Lin J., Meyers M.C., Miranda M., Narusaka M., Nguyen M., Palm C.J

Sakurai T., Satou M., Seki M., Shinn P., Southwick A., Tracy S.E.

Shinozaki K., Davis R.W., Ecker J.R., Theologis A.,

"Full Length cDNA of gene AT4919230 (GI:7268718).";

Submitted (AUG-2001) to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      InterPro; IPR001128; Cytochrome_P450.
Pfam; PF00067; p450; 1.
PROSITE; PS000086; CYTOCHROME_P450; UN.
Heme; Monooxygenase; Oxidoreductase.
SEQUENCE 467 AA; 53037 MW; 2F4230
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Arabidopsis thaliana (Mouse-ear cress).
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; Rosidae;
eurosids II; Brassicales; Brassicaceae; Arabidopsis.
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01-DEC-2001 (TrEMBLrel. 19, Last sequence update)
01-DEC-2001 (TrEMBLrel. 21, Last annotation update)
01-TUN-2002 (TrEMBLrel. 21, Last annotation update)
Putative cytochrome P450 protein.
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                        309
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                                                                                                                                                                                                                                                                                                                                                                                        LLLPSLLSLLLFLILLKRRNRKTRENLPPGKSGWPFLGETIGYLKPYTATTLGDFWQQHV 72
R-----
                                                                                                                                                        MSMDPGEEET---EQLKKEYYTFMKGVVSAPLNLPGTAYHKALQSRATILKFIERKMEER
                                                                                                                                                                                                                  HAKLRKLVLRAFMPESIRN-MVPDIESIAQDSLRSW-EGTMINTYQEMKTYTFNVALLSI 183
                                                                                                                                                                                                                                                    HRDMRSISLNFLSHARLRTILLKDVERHTLFVLDSWQQNSIFSAQDEAKKFTFNLMAKHI 192
                                                                                                                                                                                                                                                                                            KRYGSVFKTHVLGCPCVMISSPEAAKFVLVTKSHLFKPTFPASKERMLGKQAIFFHQGDY 125
                                                                                                                                                                                                                                                                                                                                SKYGKIYRSNLFGEPTIVSADAGLNRFILQNEGRLFECSYPRSIGGILGKWSMLVLVGDM 132
                                                                                                                                                                                                                                                                                                                                                                    LFAGSLFLYFLRCLISQRRFGSSKLPLPPGTMGWPYVGET---FQLYSQDP-NVFFQSKQ
                                                                                                                                                                                                                                                                                                                                                                                                                                                  164;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Similarity
                                                                                                                                      GKDEVLYREDLKRCYYILEKGYNSMPVNLPGTLFHKSMKARKELSQILARILSER
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              CYTOCHROME_P450; UNKNOWN_1
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                                                          -QNGSSH-----NDLLGSFMGDKEELTDEQIADNIIGV
                                                                                                                                                                                                                                                                                                                                                                                                                                                  96;
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Pred. No. 3e-4
%6; Mismatches
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AC QSPH
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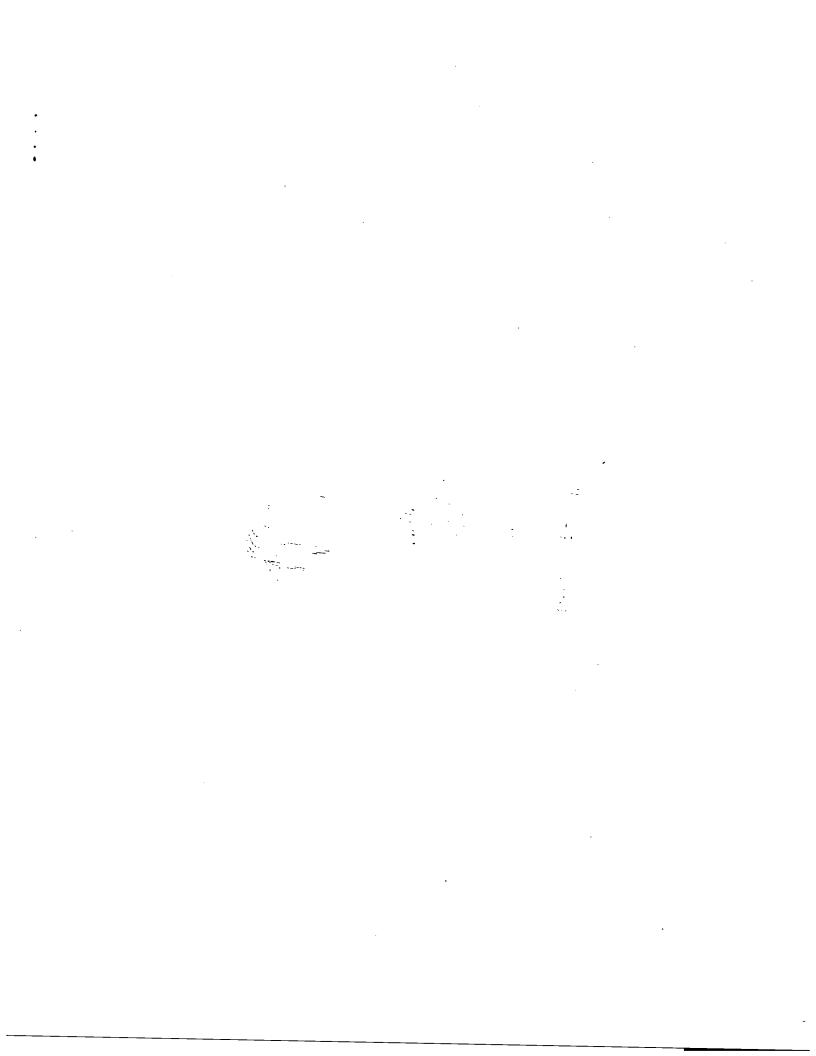
AC Q9FH76;
AC Q9FH76;
DT 01-MAR-2001 (TrEMBLrel. 16, Last sequence update)
DT 01-MAR-2001 (TrEMBLrel. 20, Last annotation update)
DT 01-MAR-2002 (TrEMBLrel. 20, Last annotation update)
DE Cytochrome P450 (AT5945340/K9E15_12).
OS Arabidopsis thaliana (Mouse-ear cress).
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; Rosidae;
eurosids II; Brassicales; Brassicaceae; Arabidopsis.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                           "Arabidopsis cDNA clones.";
Submitted (NOV-2001) to the EMBL/GenBank/DDBJ databases.
-!- SIMILARITY: BELONGS TO THE CYTOCHROME P450 FAMILY.
EMBL; AB020744; BAB10255.1;
-- EMBL; AY065065; AAL57698.1;
-- InterPro; IPR001128; CYTOCHROME_P450.
Pfam; PF00067; p450; 1
PRINTS; PR00086; CYTOCHROME_P450; UNKNOWN_1.

PROSITE; PS00086; CYTOCHROME_P450; UNKNOWN_1.
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Bowser L., Carninci P., Chang E., Dale J.M., Goldsmith A.D.,
Hayashizaki Y., Ishida J., Jones T., Kamiya A., Karlin-Neumann G.,
Kawai J., Lam B., Lee J.M., Lin J., Miranda M., Narusaka M.,
Mguyen M., Onodera C.S., Palm C.J., Quach H.L., Sakurai T., Satou N
Seki M., Southwick A., Tang C.C., Toriumi M., Wu H.C., Yamada K.,
Yamamura Y., Yu G., Yu S., Shinozaki K., Davis R.W., Theologis A.,
129 VGDMHRDMRSISLNFLSHARLRTILLKDVERHTLFVLDSWQQNSIFSAQDEAKKFTFNLM 188
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 STRAIN-COLUMBIA;
MEDLINE-20181125; PubMed-10718197;
Sato S., Nakamura Y., Kaneko T., Katoh T., Asamizu E., Kotani H.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           "Structural analysis of Arabidopsis thaliana chromosome 5. X. Sequence features of the regions of 3,076,755 bp covered by sixty Pl and TAC clones.";
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                                                       AAKQRRYGSVFKTHVLGCPCVMISSPEAAKFVLVTKSHLFKPTFPASKERMLGKQAIFFH 121
                                                                                                        QQHVSKYGKIYRSNLFGEPTIVSADAGLNRFILQNEGRLFECSYPRSIGGILGKWSMLVL 128
                                                                                                                                                                      LFLTLSAAALFLCLLRFIAGVRRSSSTKLPLPPGTMGYPYVGET----FQLYSQDP-NVFF
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31.8%; Pred. No. 3.3e-39;
tive 95; Mismatches 184
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                                                                                                                                                                                                                                                                               189 AKHIMSMDPGEEET---EQLKKEYVTFMKGVVSAPLNLPGTAYHKALQSRATILKFIERK 245
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                                                               FNPWRWQQQNNGASSGSGSFSTWGNNYMPFGGGPRLCAGSELAKLEMAVFIHHLVLKFN 484
WSIVGPSDGIQYGPFALP----QNGLPIALER 461
                      WELAEDDQ-----PFAFPFVDFPNGLPIRVSR 511
                                                FDPSRFE-----VAPKPNTFMPFGSGIHSCPGNELAKLEISVLIHHLTTKYR 433
                                                                                                   PLTYRVIQETLRAATILSFTEREAVEDVEYEGYLIPKGWKVLPLFRNIHHNADIFSDPGK 386
                                                                                                                    DFTQCVINETLRLGNVVRFLHRKALKDVRYKGYDIPSGWKVLPVISAVHLDNSRYDQPNL 424
                                                                                                                                                        IIGVIFAARDTTASVLTWILKYLADNPTVLEAVTEEQMAIRKDKKE-GES-LTWEDTKKM
                                                                                                                                                                       ILSLLFAGHETSSVAIALAIFFLQACPKAVEELREEHLEIARAKKELGESELNWDDYKKM 364
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Search completed: March 30, 2003, 12:06:27 Job time: 66 secs

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AF044216 Arabidops AL132979 Arabidops AF273674 Plasmodiu

Description

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Post-processing: Minimum Match 0% Maximum Match 100% Listing first 45 summaries
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Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
Rosidae; eurosids II; Brassicales; Brassicaceae; Arabidopsis.

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        Choe, S.,
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Dilkes, B.P., Fujioka, S.,
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22-alpha-hydroxylase (DWF4) gene,
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AC127730 Rattus no
AC016220 Homo sapi
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Minimum Maximum

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length: 0 length: 2000000000

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Scoring table:

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Title: Perfect score:

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Database

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Takatsuto, S.,

Sakurai, A. and

PLN 25-JUN-2001

em\_htgo\_mus:\*
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VRKQRTDDDLLGWVLKHSNLSTEQILDLILSLLFAGHETSSVAIALAIFFLQACPKAV
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join(1133. 1353,1434. 1758,1844. 1996,2095. .2409,
2562. 2654,2746. .2824,2931. .3040,3795. .4040)
/gene="NWF4"
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/db_xref="GI:2935342"
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/chromosome="III"
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2562. .2654,2746. .2824,2931. .3040,3795. .4398)
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ATT3A5/c
LOCUS
DEFINITION Arabidopsis thaliana DNA chromosome 3, BAC clone T3A5.

ACCESSION AL132979
VERSION AL132979.2 GI:6782244
KEYWORDS
SOURCE Arabidopsis thaliana
ORGANISM Arabidopsis thaliana
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
ROSIGNAE; eurosids II; Brassicales; Brassicaceae; Arabidopsis.

REFERENCE 1 (bases 1 to 84196)
AUTHORS Bloecker, H., Mewes, H.W., Lemcke, K., Mayer, K.F.X., Quetier, F. and
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FEATURES
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On Jan 27, 2000 this sequence version replaced gi:6434247.
Information on performance of analysis and a more detailed annotation of this entry and other sequences of chromosomes 3, 4 and 5 can be viewed at: http://www.mips.biochem.mpg.de/proj/thal/.
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EU Arabidopsis sequencing,project.
Direct Submission
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QATNRGGIVAANSACASETSVVIVRRRDSPPVEEQCQIEEEDSSVSCCSTSEEKSKRR
IEFVDLEENNGDDRETETSWIYDDLNKSEESMNMDSSSVAVEDVESRRRLRKSLHETV
                                                                                                                                                                                                                                                                                                                                                 /gene="T3A5.10"
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/gene="T3A5.10"
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/gene="T3A5.10"
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/protein_id="CAB62432.1"
/db_xref="GI:6561966"
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/gene="T3A5.10"
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/chromosome="3"
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|2339. .13197
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/variety="Columbia"
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complement(28289.
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PSSFFTLPGSGFSDFFQYTNDBGFHFPHLEHHQNAAVASEEFDSDEWMESLINGGDAS
QTNPDFF1YGHDFFVSFPSRLSAFSYLNRVNKDDSASQQLPPPPASTTAIWSBSPPSPQ
HPPPPPAQDDFDLNQPIFKAIHDYAFKPETKPDTLIRIKESYSESGDPIQRWGYYFAF
ALSHKSTESPSSSSSSEDEFTLSYKTLNDACPYSKFAHLTANQAILEATNQSNNIHI
UDEGIFQGIQWSALLQALATRSSGKFT&RISGIPASLGDSFGPSLIATGRHRDFA
AILDLNESFYPUTFIQLLNGSSFRTUPDEVLVVNEWLELYKILDETATTVGTALRLA
AILDLNESFYPUTFIQLLNGSSFRTUPDFALVNEWLELYKILDETATTVGTALRLA
ASLNPRIVTLGBYEVSLNRVEFANRVKNSLRFYSAVFESLEPNLDRDSKERLRVERVL
FGRRIMDLVRSDDDNNKPGTREGLMEEKEQWRVLMRAGFEPVKPSNYAVSQAKLLLW
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27478. .27570,27723. .28037,28136. .28288,28374. .28698,
28779. .28999))
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/gene="T3A5.40"
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SLRPILLSSSSFSTKGTWRELLGLKRTHVRSKKTDKVNEEVLSQDHKIISGNVATREC
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/db_xref="GI:6561968"
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                                                                                                                         TATTTTGTTGTGGAAGTAGTAGTAATATACATTAAGCAAATTTAAAAAAATTATATAA 180
GGTTTGACTGTCCAGTTCGGTAATAATCTAATAACTCTGTCTTTGACCGCACGCTCGTGT
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38307. .41323
38307. .41323
/gene="T3A5.50"
/gene="T3A5.50"
/gene="T3A5.50"
complement(join(38307. .38796,38877. .39090,39189. .39270,40180. .40242,40337. .40401,40489. .40564,40655. .40734,40805. .40919,41225. .41323))
/note="Contains Eukaryotic putative RNA-binding region RNP-1 signature AA179-186"
/codon_start=1
/product="U1 snRNP 70K protein"
/protein_ia="CaB62436.1"
/db_xref="G1:6561970"
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NLLKLEEPREPLEYKPPPEKRRCPPYTGMAQFYSNRAEPGDDEYKAPPKPEVELLPSQKR
ERIHKLRLEKGVEKAAEDLKKYDPNNDPNATGDPYKTLFVSRLNYESSESKIKEFES
YGPIKRVHLYTDQLTNKPKGYAFIEYMHTRDMKAAYKQADGQKIDGRRVLUDVERGRT
VPNWRPRRLGGGLGTSRVGGGEEIVGEQQPQGRTSQSEEPSRPREEREKSREKGKERE
KSRELSHEQPRERSRDRPEEDKHHRDRDQGGBDRDRDSRRDRDTRDBGDRDRDRDR
GRDRTSRHDBADRSKKERENYEGGEYEHEGGGRSRENDAEYRGEPEETRGYYEDDQGD
TDRYSHRYDKMEEDDFRYEREYKRSKSESREYVR"
complement (38307. .38796)
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complement(40243.
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complement(28374.
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Pred. No. 1.9e-178;
D; Mismatches 0;
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GAGAGAGAGAGAAACTAGCTCC
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                                                                GAAGCTCATTGGTTAGGTTTAAGCTTAATAAGAAGATTTTATTAAATTTTAATGACGATG
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PUBMED REFERENCE AUTHORS TITLE JOURNAL ACCESSION VERSION KEYWORDS SOURCE ORGANISM RESULT 3 AF273674 LOCUS REFERENCE AUTHORS DEFINITION JOURNAL MEDLINÇ TITLE 2 (bases 1 to 4629)
Li,J., Maga,J.A., Cermakian,N.,
Direct Submission Plasmodium falciparum Eukaryota; Alveolata; Apicomplexa; Haemosporida; Plasmodium. Eukaryota; Alveolata; Apicomplexa; Haemosporida; Plasmodium. 1 (bases 1 to 4629)
Li, J., Maga, J.A., Cermakian, N., Cedergren, R. and Feagin, J.E. Identification and characterization of a Plasmodium falciparum RNA polymerase gene with similarity to mitochondrial RNA polymerases Mol. Biochem. Parasitol. 113 (2), 261-269 (2001) AF273674
4629 bp DNA linear INV 24-APR-2001
Plasmodium falciparum DNA-dependent RNA polymerase (TRNAP) gene,
complete cds; nuclear gene for probable mitochondrial product. Submitted Plasmodium AF273674.1 GI:9857984 falciparum Seattle 4629 bp Biomedical Research Cedergren, R. and Feagin, J. Institute,

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HNIDERGRMYFLSPHLHHMSDDICRSLITFAEQKEIGNKGLFWLKIHLANTFGKDKLS
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KHUCANRQELQLSDUKKESUFCQKQREKLMRKEIILYRSKRDRUKIELPVFIHSYVWK
NUNWYGVIHMRECCANYLLUNAIUSHIPLUYLPMICKPKRWENPEGGMLLLKUSFIRC
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/db_xref="taxon:5833"
/chromosome="11"
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<70. .>4581
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/db_xref="GI:9857985"
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AE001372.1 GI:3845094
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1 (bases 1 to 12029)
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GQDQAHHHHHHHHHQLQPQQPQGTVANPPSNEPVKTQVFREAKPGGFKAYEEKYES
KHYKLKENVYDGKKDCDEKYEANYAFSEECPYTVNDTSQENGPNIFALRKRFPLGMN
DEDEGGKEALAIKDKLPGGLDEYQNQLYGICNETCTTGGPAALDYVPADAPNGYAYGG
SAHDGSHGNLRGHDNKGSEGYGYEAPYNPGFNGAPGSNGMQNYVPPHGAGYSAPYGVP
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KKHKNNEDAESYVSKKHKSHDCEKKGSKKOSKKKDNDEDAESYKSKKSVKEKDHDGEKKKS
KKHCNNEDAESYVSKKHKSHDCEKKGSKHKDNEDAESYKSKKSVKEKDHDGEKKKS
KKHTNEDAESYVSKHKHKSHDCEKKGSKHKDNEDAESYKSKKSVKEKDHDGEKKKS
KKHTNEDAESYKSKHKSHCHOKHONDEDAESYKSKKSVKENDAATPG
SKKTNEENKNKEKTNNSKSDGSKAHEKKENETKNTAGENKKVDSTSADNKSTNAATPG
SKKTNCGGKKTDKTGASTNAATNKGQCAAEGATKGASTSKEATKEASTSKEATKE
                                                                                                                                                                                                                                        AANNGEQVMSRGQAQLQEAGKKKKKRGCCG"
complement(7684...8322)
/gene="PFB0105c"
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/gene="PFB0100c"
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/gene="PFB0100c"
/product="hypothetical protein"
/protein_id="AAC71811.1"
/db_xref="GI:3845096"
                                                                                                                                                                        complement(7684. .8322)
/gene="PFB0105c"
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/protein_id="AAC71810.1"
/db_xref="GI:3845095"
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/chromosome="2"
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Submitted (24-MAY-2002) Genome Analysis, Institute of Molecular Biotechnology, Beutenberstr. 11, Jena 07745, Germany CDS predictions from GeneID may contain errors. Further Information is available from IMB Jena, Department of Genome Analysis (http://genome.imb-jena.de/dictyostelium/) and the Univerity Colonge, Institute for Biochemistry I (http://www.uni-koeln.de/dictyostelium/project.shtml
                                                                                                                                                                                                Submitted (06-APR-2002) Genome Analysis, Institute of Molecular Biotechnology, Beutenberstr. 11, Jena 07745, Germany 3 (bases 1 to 129360)
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AX4, *** SEQUENCING IN PROGRESS ***, in
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YSHSLLEDKFNNMKSSLWSIGKLAHEHKLPFKIKMKKWWKCGGHVTDELLIKEHDDY
NSIYNYINNESSSREQELIFLAMIKHSWTTFTMETFIKCKISLENNMRNVTN"
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NOTE: This is a 'working draft' sequence.
This sequence will be replaced
by the finished sequence as soon as it is available
the accession number will be preserved.
                                                                                                                                                                                                                                                                                                                     FRFMTHTKSIPFLNADSLYFIVMKFDNIDRIEEIIQFLLLERCEVTVLKLLEVAIESG
RIETVNYLLSNYLQELTNQGPLKTYYTIFQFNNLSILNIFLSNEIYKSLLALYEINSE
IQYSDSESFKFINGTYEKDFYNKSFKYGYLSICKLLEBHYGSNNNNNQDNNSENSSSN
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IIFLEKSKGDRRIS KLENYEINKEDEKMLDLIKGSIRANNITAKFESGGDNEENDG
YQLQIYPSTLKCALLSKDLEIIKYIENNLILIKNIENBFGIGLNGLLKIITTTTTTT
TTTTTTTTATTIKQNKDNEIIEFLIEKFQSIDSDQLKETIDLNYLIMETKNYELIDKI
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                                                                                                                  /note="ORF_ID:dd_02315"
/codon ataut-
                                                                                                                                                                                                                                                                                                          KYKEYQIKVPHGFYQIFNYLYLKSPSLAHFTMETWDLFQYGYFRVNRYLNDSHFTFDY
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/translation="MANNNNNNNNNNNNENKNEYLFWKVFKNKYLIKNIFYQMTIENNEFN
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/note="ORF_ID:dd_02309"
    EKLNRNSNGGYVELTPISQSKRQRKNIGNRLVRPCDCKGTQRHVHVKCLCEWIGKCNK
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/db_xref="GI:21166069"
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/note="ORF_ID:dd_02310"
                        'translation="MLIECRECLEEIEVEDPIYDKKEFNLNENSIKSKDIEIEELEFK
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/Translation="msgirissperksiestingkdksinlnnndniknnnnnnsiknn nnnnksiknn knnnnnssiknn knnnnnssiknn knnnnsser for statten perkgdy iesdelksmliidde ndden knnnksbudtereggedden for statten perkgdy en knnnksperksperksperksperksperkgder for hedde for statten for stat
VIPPITNSKTYVVTANLSVNYKKFVVLESFSSVETRIQKRDGKKIFISSTIKDQNGVI
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TNKPIYIAINWKGVS"
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LGSLVGSVEKLRNLSTINSVPLILSPYEIRLGLEKQWFQIINESATFPTITDHNLSLF
KESRQTYYQSLMDKYKEQRLKKEKEFRNKLNYNSNSNKNKNKNKIPSLDTTDSNNNNN
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COMPLEMENT (join(15910. .15915,16125. .16229,16310. .16392,
16502. .16576,16692. .16710))

/note="ORF_ID:dd_02326"
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/translation="MMIDKVFKLAKGFFGRSKNCKSLARERVEKGLEYNYVSRKLKKR
DFRKMWIERINAGAROHEMTYSDFQRGLIASGVEINRKVLLFSIGAVSEPFSFKVLVD
HSKNTVSNLHPKSYIPLOPKN"
complement(join(14375. .14423,14526. .14851))
/note="ORF_ID.dd_02323"
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/protein_id="AAM43695,1"
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/protein_id="AAM43694.1"
/db_xref="GI:21166077"
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/protein_id="AAM43693.1"
/db_xref="GI:21166076"
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/protein_id="AAM43692.1"
/db_xref="GI:21166075"
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LQNIYIAHQKYHRVTIADSFKNIFCTLIPVKRFCY"
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MLMLPSTLPQONSKIYYGYDTILNNHINNNNNNGVGSGSGGSGTGGATVNSLLFNNF
NGGIISFSNEVSGGGMFMNYNPLVGINGDTTTAGYNPGFLNSPSYSYYSFYPSSSSPS
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/protein_id="AAM43691.1"
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/protein_id="AAM43690.1"
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Query Match Best Local Matches 41 CDS

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LEGSLGVKGENYLWDALQINSDHRALMVVVIFLFWLFYIGLNLFAVEYFDWTSGGYTH
KVYKRGKAPKLNDVEEERNQNQIVKKATDNMKOTLKNHGGLESWKSISYTVPVAGTNK
LLLDDIMGWIKPGGMTALMGSSGAGKTTLLDYLAKRKTMGTTYTGESLLNGKQLEIDFE
RITGYVEQMDYHNPGLTVREALRFSAKLRQEPWVPLKDKYQYYEHYLEMBEMHHLGDA
LIGTLETGVGISVEERKRLTIGVELVAKPQLIFLDEFTSGLDAQSSYNIIKFIRKLAD
                                                                                                                                  AGMPLYCTHOPSSYLFEHEDRILLLARGĞKTYYFGDIGDKSKTLTSYFERHGYRPCT
ESENPAEY ILEATGAGIHKKTDVMPPEMKOSSEYQNYVNELDLITKEELGKYILDS
DLQVDGKQAPPREFANGFLTQFIEVYKRLINIYYRDVFYTMGSFAQSAVSGLVIGFFY
YDLKNSSSDQQQRIFMSWEAMILGVLLIYLVLPMFFIQKEYFKRDTASKYYSWHAFSL
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WGDKETLTSRELTILVLSFIFGGIYFQQPLTTDGLFTRGGAIFTSIIFNCILTQGELH
GALSGRRILQKHKSYALYRPSAYFVSQILIDIPFILVQVFLHSFIVYFMYGFEYRADK
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DYDSINNIEEKFENVSKELEGQSIKFREIDGGKNNNNHDIELGERKPENEEDFKLRQY
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KDKNKINTFNILNDINAFIEDGKMLLVLGRPGAGCSTLLRVIANQRESYISVDGDVTY
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663 TAATGACTTTTTTTTTTTTCTACCACGGTGGATGAAAGTTATAGTACTATTAGCCAGAGACA 722
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                                                                 GATTCTGCTGGAGCATTTATCAAAAATTATTAGCACGAATGGGTTTATTAATTTAAAAAAC 602
                                                                                                                           CCTAAGGGTAATTTTGGAAATCCCAATTTAAACCGATTGAGACCGTACCGGACTTCCTGG
                                                                                                                                             ATTTCCTAAGTCCGCCTGGTGTTGTCCTATGAAATTATAAATGGTGTAAATTTCTGTAAT 18785
                                                                                                                                                                                                        TTTGACTGTCCAGTTCGGTAATAATCTAATAACTCTGTCTTTGACCGCACGCTCGTGTAG 422
                                                                                                                                                                                                                          AGTAAATGTGTTTTCTGACTATTGAGGGGCAAAAAAAGACAATGCCAAAAGTCTACGGG 362
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JOURNAL
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AUTHORS
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Direct Submission Submitted (05-NOV-2001) Adam G., Pflanzenschutz, Institut fuer ANgewandte Botanik, Ohnhorststrasse 18, 22609 Hamburg, GERMANY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Heinze, C., Willingmann, P. and Adam, G. Short intergenic regions of the S RNAs of Tomato tospovirus -not a species characteristic
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Tomato spotted wilt virus.
Tomato spotted wilt virus
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/fibm xief="MSSSYVESIIQTRASVWGSTASGKAVVDSYNIEDSYLALSYCS
NTVNTNGVKHQGHLKVLSPDQLHSIGSTMNRSDIKDRFQLQEKDIIPNDRYIEAANKG
SLSCVKEHTYX IETCYMQALGKVNVLSNRNYHEWLYSFKPLSFKQVESNRRTVNSLAV
RSLLTSAENNIMNSQAFVASTDSHKKLSLMLRVFKVLRQVSIQKLFKVAGDETNKT
FYLSIVCIPNHNSVETALNISVICKHQLPIRKCKAPSELSMVFSDLKEPVNIVHDPSY
PQRIVHALLETHTSFAQVLCNNLQEDVIIYTLNNYELTPGKLDLGERTLNYSEDICKR
KYFLSKTLECLPSNTQTMSYLDSIQIPSWKIDFARGGIKISPQPVSVAKSLLKLDLSG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ssRNA negative-strand viruses; Bunyaviridae;
/product="N protein"
/protein_id="CAD11446.1"
                                                                                   complement(2436.
                                                                                                                                         IKKKGSKISDGYASGSK"
                                   /codon_start=1
                                                  /gene="N"
/function="structural protein"
                                                                                                                                                                                                                                                                                                                                                   /codon_start=1
                                                                                                                                                                                                                                                                                                                                                                 /gene="NSs"
                                                                                                                                                                                                                                                                                                                                                                                                     /gene="NSs"
                                                                                                                                                                                                                                                                                                                                                                                                                                                     /specific_host="virginia
/db_xref="taxon:11613"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         /organism="Tomato
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                                                                                                                                                                                                                                                                                                                                                                                                                                     country-"Bulgaria"
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                www-shgc.stanford.edu
Quality: Phrap Quality >-40 99.7% of Sequence;
Estimated Total Number of Errors is 2.7.
Location/Qualifiers
1. .171317
                                                                                                                                    Direct Submission
Submitted (01-JUN-2001) DOE Joint Genome Institute, 2800 M
Drive, Walnut Creek, CA 94598, USA
On Jun 1, 2001 this sequence version replaced gi:12830142.
Draft Sequence Produced by DOE Joint Genome Institute
                                                                                                                                                                                                                                          Submitted (12-JAN-2000) Production Sequencing Facility, Genome Institute, 2800 Mitchell Drive, Walnut Creek, CA 3 (bases 1 to 171317)
                                                                                                                  www.jgi.doe.gov
                                                                                                                                                                                                                      DOE Joint Genome Institute and Stanford Human Genome Center
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Joint Genome Institute.
 /organism="Homo sapiens'
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2800 Mitchell

DOE Joint 94598, USA

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Local Similarity
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DOE Joint Genome Institute and Stanford Human Genome Center.
                                                                                                                                                                                    Homo sapiens chromosome 5 clone
AC020941
AC020941.5 GI:14277273
Direct Submission
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IKKMSVISCLfffknrgsimkvikqsdfffgkitikkfsdrigatdmffrfldsmirv
RLVEETGNSENLNTIKSKIASHPLIQAYGLPLDDAKSVFLAIMLGGSLPLIASVDSFE
MISVVLAIYQDANTKDLGIDPKKYDTKEALGKVCTVLKSKAFEMNEDQVKKGKEYAAI
LSSSNPNAKGSIAMGHYSETLNKFYEMFGVKKQAKLTELA"
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48.2%;
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'db\_xref="taxon:9606"

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Muzny, D.M., Adams, C., Adio-Oduola, B., All-osman, F.R., Allen, C., Alsbrooks, S.L., Amaratunge, H.C., Are, J.R., Ayele, M., Banks, T., Barbaria, J., Benton, J., Bimage, K., Blankenburg, K., Bonnin, D., Burbaria, J., Benton, J., Bimage, K., Blankenburg, K., Bonnin, D., Burbaria, J., Benton, J., Brieva, M., Brown, E., Brown, M., Bryant, N.P., Buhay, C., Burch, P., Burkett, C., Burvell, K.L., Byrd, N.C., Carter, M., Cavazos, S.R., Chacko, J., Chavez, D., Chen, G., Chen, R., Chen, Z., Chowdhry, I., Christopoulos, C., Chen, G., Chen, Z., Coyle, M.D., Dathorne, S.R., David, R., David, M.L., Davis, C., Davy-Carroll, L., Dederich, D.A., Delaney, K.R., Delgado, O., Denn, A.L., Ding, Y., Dinh, H.H., Delaney, K.R., Delgado, O., Denn, A.L., Ding, Y., Dinh, H.H., Douthwaite, K.J., Draper, H., Dugan-Rocha, S., Durbin, K.J., Earnhart, C., Edgar, D., Edwards, C.C., Elhaj, C., Escotto, M., Falls, T., Ferraguto, D., Flagg, N., Ford, J., Eoster, P., Frantz, P., Garis, M., Ganer, T., Garza, N., Gill, R., Gorrell, J.H., Guevara, M., Gunaratne, P., Hale, S., Hamilton, K., Harris, C., Harris, K., Hart, M., Havlak, P., Hawes, A., Hernandez, J., Jackson, E., Harris, K., Hart, M., Haylak, P., Hawes, A., Hernandez, J., Jackson, E., Hallyk, S., Hume, J., Jackson, L.E., Jacobson, B., Jia, Y., Johnson, R., Jolivet, S., Joudah, S., Karlsson, E., Kelly, S., Khan, U., King, L., Korvah, J., Kovar, C., Krattovic, J., Kureshi, A., Landry, N., Leal, B., Lewis, L.C., Lewis, L., Li, J., Li, Landrage, O., Lieu, C., Liu, J., Liu, M., J., Loutageed, H., Louder, R., Lucier, R., Luna, R., Ma, J., Maheshwari, M., Mapua, P., Marttin, R., Martindale, A., Martinez, E.,
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Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae;
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Rattus norvegicus clone CH230-3H24,
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(see http://www.hgsc.bcm.tcm.edu/docs/Genbank_draft_data.html).

* NOTE: This is a "working draft' sequence. It currently

* consists of 60 contigs. The true order of the pieces

is not known and their order in this sequence record is

* arbitrary. Gaps between the contigs are represented as

* runs of N, but the exact sizes of the gaps are unknown.

This record will be updated with the finished sequence

* as soon as it is available and the accession number will

* be preserved.
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Direct Submission
Submitted (09-JUL-2002) Human Genome Sequencing Center, Department of Molecular and Human Genetics, Baylor College of Medicine, One Baylor Plaza, Houston, TX 77030, USA
On Jul 9, 2002 this sequence version replaced gi:17941008.
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Sequencing vector: M13;
Chemistry: Dye-terminator Big Dye: 100% of reads
Assembly program: Phrap; version 0.990329
Consensus quality: 175720 bases at least Q40
Consensus quality: 180089 bases at least Q30
Consensus quality: 180792 bases at least Q20
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Web site: http://www.hgsc.bcm.tmc.edu/
Contact: hgsc-help@bcm.tmc.edu
------ Project Information
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Submitted (16-AUG-2002) Wellcome Trust Sanger Institute, Hinxton, Cambridgeshire, CB10 1SA, UK. E-mail enquiries: humquery@sanger.ac.uk Clone requests: clonerequest@sanger.ac.uk On Aug 21, 2002 this sequence version replaced gi:22204483.
                                                                                                                                                                                                                                                                                                                              AL732314 224635 bp DNA linear HTG 17-1
HOMO sapiens chromosome X clone RP13-465B17, *** SEQUENCING
PROGRESS ***, 8 unordered pieces.
                                                                                                          Direct Submission
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Mammalia; Eutheria; Primates;
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Center: Wellcome Trust Sanger Institute Center code: SC

Web site: http://www.sanger.ac.uk Contact: humquery@sanger.ac.uk

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Insert size: 183401; 20.9% error; agarose-fp
Quality coverage: 6.54x in Q20 bases; sum-of-contigs Quality
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3853 3952: gap of 100 bp
3953 36565: contig of 32613 bp in length
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36666 70753: contig of 34088 bp in length
70754 70853: gap of 100 bp
70854 141740: contig of 70887 bp in length
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Plasmodium falciparum MAJ3P7, complete sequence.
AL034559 AL008974 AL008975 AL008981 AL008983 AL009015 AL010138
AL010143 AL010146 AL010154 AL010157 AL010160 AL010165 AL010169 AL010189 AL010207 AL010208 AL010214 AL021885 AL021888
AL139179 Z98556 Z99557 Z98558
AL139179 Z9856 Z99557 Z98558
                                                                                                                                                  On or before May 14, 2001 this sequence version replaced gi:2982540, gi:2982541, gi:2982558, gi:2982558, gi:2982554, gi:2982564, gi:2982564, gi:2982564, gi:2982566, gi:2982564, gi:2982568, gi:2982569, gi:2982569, gi:2982569, gi:29825974, gi:2982592, gi:29825974, gi:2982598, gi:2982597, gi:2982598, gi:2982597, gi:2982597, gi:2982598, gi:2982599, gi:2982597, gi:2982598, gi:2982599, gi:2982597, gi:2982598, gi:2982599, gi:2982597, gi:2982598, gi:2982599, gi:298259, gi:298259, gi:298259, gi:2982599, gi:298259, gi:298259, gi:298259, gi:298259, gi:2982599, gi:298259, gi
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Eukaryota; Alveolata; Apicomplexa; Haemosporida; Plasmodium.

1 (bases 1 to 253305)

Bowman, S., Lawson, D., Basham, D., Brown, D., Chillingworth, T.,

Churcher, C.M., Craig, A., Davies, R.M., Devlin, K., Feltwell, T.,

Gentles, S., Gwilliam, R., Hamlin, N., Harris, D., Holroyd, S.,

Hornsby, T., Horrocks, P., Jagels, K., Jassal, B., Kyelso, S., McLean, J.,

Moule, S., Mungall, K., Murphy, L., Oliver, K., Quail, M.A.,

Rajandream, M.-A., Rutter, S., Skelton, J., Squares, R., Squares, S.,

Balston, J.E., Whitehead, S., Woodward, J.R., Newbold, C. and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            protein; histone H2A variant; kinešin related protein; N-acetylglucosamine-1-phosphate transferase; protein kinase; R-(repat; R-RA) repeat; repll; rep20; rifin; RNA-binding protein; stevor; T-complex protein 1 epsilon subunit; telomere; var.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Submitted (17-DEC-1998) P.falciparum Genome Sequencing The Sanger Centre, Wellcome Trust Genome Campus, Hinxto
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         acylaminoacyl-peptidase; ATP-dependent RNA Helicase; elongation factor; F49C12.11-like protein; HesB-like
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Direct Submission
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Oliver, K., Bowman, S.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      The complete nucleotide sequence of chromosome 3 of Plasmodium
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Barrell, B.G.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Lawson, D., Bowman, S.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Nature 400 (6744), 532-538 (1999)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       (bases 1 to 253305)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      (bases 1 to 253305)
/organism="Plasmodium
                                                                   1. .253305
                                                                                                                   ocation/Qualifiers
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      falciparum 3D7'
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/chromosome="3"
/clone="MAL3P7"
458. .4060
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     aa; Similarity eg to C.elegans RNA-binding protein (TR:Q18318) BLAST Score; 378, sum P(1) = 3.8e-35; 378 identity in 297 aa overlap, predicted using hexExon, Pfam match to PF00076 rrm, RNA recognition motif. (a.k.a. RRM, RBD, or RNP domain) Score 58.01
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             RANKVSSRSHAILQIYVYNĒILDDNMNTISYKAKLCFVDLĀGSERASATSNKĢĒRĒKE GSYINQSLLALANCINSLASHRNISKVRVKYRDSKLTHLLKNSLEGNCLVWHĀNINP SRTSFQESNNTLKYAFRARNIKLCATVQTMDNKESDIEK LIKKNENLQKEYDTLLGKY TNLKEFFFIINVINQLYKKQISCYKLIENISDMNSSMELKQDITMYDQLYKMKSDEYR KKVDSKELKQDITMYDQLYKMKSDEYR KKVDSLKDLYQEEKQFLNNLFDTFLEKNLNYVINSKDLVRDINKSLLEEMIFFKHNENK VNENFLYNGEVVAVDENVAVDENVAVDENVAVDENVAVDENVAVDENVAVDENVAVDENVAVDENVAVDENVAVDENVAVDENVAVDENVAVDENVAVDENVAVDENVAVDENVAVDENVAVDENVAVDENVAVDENVAVDENVAVDENVAVDENVAVDENVAVDENVAVDENVAVDENVAVDENVAVDENVAVDENVAVDENVAVDENVAVDENVAVDENVAVDENVAVDENVAVDENVAVDENVAVDENVAVDENVAVDENVAVDENVAVDENVAVDENVAVDENVAVDENVAVDENVAVDENVAVDENVAVDENVAVDENVAVDENVAVDENVAVDENVAVDENVAVDENVAVDENVAVDENVAVDENVAVDENVAVDENVAVDENVAVDENVAVDENVAVDENVAVDENVAVDENVAVDENVAVDENVAVDENVAVDENVAVDENVAVDENVAVDENVAVDENVAVDENVAVDENVAVDENVAVDENVAVDENVAVDENVAKEKKKKIPINMETKKRTMNGTKDPIHKTPYDINIVGILAKEDVSNKSNDYNTNKNIEKNNY
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GINCTVFAYGATGSGKTYTMLDDKNQNGIVQLSLLELFTIINEKKCRNIKVLMSFLEV
YNETIRDLLGKEKNKTLEVQEDVAEVKVSNLCEIEVNNYEQAMLLINEGVKNRKMSPT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     /note-"PFC0860w (MAL3P7.1), Kinesin-related protein, len: 1200 as; similarity: to kinesin-related protein. D.melanogaster kinesin-like protein (TR:P91945) BLAST Score: 664, sum P(2) = 1.9e-67; 28% identity in 707 aa overlap, predicted using hexekon, Pfam: match to PF00225 kinesin, Kinesin motor domain Score 311.54"
                                                                                                                                                                                                                                                                                                                                                                                                                                                             /db_xref="SPTREMBL:097318"
/translation="MGLFDKIRNIEKLNEAELKNIGNNDSSWHDQYRDSSYIYIGNLD
NRLTEGDIVIVFSQYGEPIDVNLVRDNETGKSKGYCFLSYADQRSTILAVDNFNGYKL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 /product="putative RNA-binding protein"
/protein_id="CAB39067.1"
/db_xref="GI:4494008"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                DDDTIKNMNSNKISDKHNMKSNNILNNENGKINDKSKKCKNINNNNNNNNNNNNNNNNNNN
NNNNNNNSSSSSGKVDGINILNNSNTNERLHTFSGVYSLNLNDEIKIEINKKDMEKN
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VYPNINGEPSTSVENITNGEHFINGQYDALKNMSLNNYDHQHNNIMNNISNKNKLFVL
                                                                                                                                                                                                                                                                                                                                                                                             LERPLVVDHILNYRLPKKYLKDADKNEYKPTGAEGQGIGVYNVVESEIKLSKVFDKIK
NKSNEEKKKKLLDEDELWALNFEKSIKKDIISPIGHDEKSRHNEGMKEEEEDEDDEDD
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         /gene="PPC0865w, MAL3P7.2"

Join(5457.5689.577,5689.577,5689.6077,6189.6743)

Joine="PPC0865w, MAL3P7.2"

/note="PPC0865w, (MAL3P7.2), RNA-binding protein, len: 309
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        /note="potential splice donor at 3' indicate splicing" 501(5457.5689...5787,5923... /gene="PFC0865w, MAL3P7.2"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            4057
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    EKKGEYNPFHNNLTDMQNSILYNIINNNVENSPHSPRMKKNVAKMLLKGNLNTANFIL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                NYTNIHNNNNNMNSNPTSSVTSKKNENNNLINTLNAYSNVKVAVRIKPIGESEENIVS
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/protein_id="CAB39023.1"
/db_xref="GI:4493964"
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458. .4060
                                                                                                                                                                                                                                                                                                                         EKDKKSHKRRHKHSYDKYSSRSRSYSTSSSTDR"
                                                                                                                                                                                                                                                                                                                                                             DDEDDDDDDSVD1KYKRHKEKRKSLTTKKYDKKEKHKRKSDHRDKHRRRENHSRHREK
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         /codon_start=1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            /gene="PFC0860w,
/note="potential
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                .4062
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ovential splice donor at 3' end splicing"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        MAL3P7.1"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        end of PFCo860w may
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Pfam:
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misc_feature
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VLSQEKIMSALMKKGVIKSPRKVANNFVDGYNVGRISSHESSINDKKKDNNONDND
VLSQEKIMSALMKKGVIKSPRKVANNFVDGYNVGRISSHESSINDKKKDNNONNONDN
NNKNNSVDIIDHLEDLIVNINEFTNURDIIKKNIIKRIKGGRNENNKOFIFPNENHI
YCTYKINELESLKKLLCVLNKKFYNILTYQLKTIDIYYTYIYIYLNEKKKLLKNIQDK
DIKYLIELDPLEFLFFQNFKYFNELNNLLLMKNNHMQPISYNFAYLRDILVRRONENKN
IINSTNINDDNYDYDINWYNNKYKYKNNNNNNSFYNRNDDYBLTDIEENISSKKKN
KFIEKEFSYNTYRNNKNNDENDEYGEYNNYDDNMIMSFYSLLIKKKNIKKNINSYDKILKKK
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YSTISSNHLKQSTINFILYKNDMNNNETLGYNKYNLNDNIKKNLNNSYDKILKKLE
YKODNAEESHINNDHNDIKOILKKLLMNEYNYNKILHENSFNYYNSTINSLLQKYC
LKEKINYIDEPLIEDNLYDSINNYLEKKANHENEISLGTPALITEKKADNSDNKEDV
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     CCLK INKYYYYSWLLFYFIILFFYNII FTLVVYFYVYKCLMNYFILFFLIYFFLMNS
LLFTII COMOFSNISSINYIAFTLLFELFSSFRLII HSGASNILFFYLLIIFFLIYFRKKMN
LLFTII COMOFSNISSINYIAFTLLFELFSSFRLII HSGASNILFFYLLIIFFYLLIIPHSSFCLS
LDFIFILIKNNIK IDYKOLFIKFENISLMHLIIGSIVSFYLLIGILMYIIIYKKKKMN
MLNTKYBGKSKSITNDKRKKSOOKTISLMHLIIGSIVSFYTHOLKDNSDFMLEGSDE
DDTCYELDTLHKKQVNSOMCLRIEKIRNDRESNGHPYDIPMIPLHNNINNINNI
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KNDLEISYCSONVILYENLTFYETIKIFLLYYNKNVDKYLNKKRTLKIMNDLDLDLYQYL
NDQIKNLMDEVKKISIFICFIVKRDTYILDEPFIALDIKTKYKKTKTKNNDLTKNNINNIN
                                                                                                                 FHEHEMRDEY INITYPELSIVIFFCVFEERFKNEIENRKIFENPHYDQYIHYFQILLLE
YLYYFIYILCLFIVLYIFDYKEFLFMSFFCFLLLYGNIFLSICLFSSLYLHSYLLFL
FENFIFCGIISIVIYVLVILSYSYNNEILINLSHVLVCIFFIFDSFALSHVLNIRSLC
LNYKRHMKHIDEDIMYEDMSNSNNFVIFGCFKKVYNQLSGDNNLNISDGIQSVCEDSN
                                                                                                                                                                                                                                                                                                                                                          ETLETRNDTDVNKEVEI NINLFYNYTSIHSYAYYTNSLFNMLSDFQNILNKKSGNKNI
ILDGSTYDNIKVVEDVKGNCDMNTLLYDKENKYNYLIKDIDNKNIREECNANFRLSKN
VSYNNNEEEEDINGNINYNDSNNIYITPKKNNKEEENNFLVKKLKKRIDTLNEPFNIK
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           YFFNDININLKONFINFNTVDDLSFNIYFNEWYYFSFFIVLEYQFNSFILNYNADILK
KNNLLTPRYDEINELNKEREITMEYKKTDEKEYQVNNEYINENVGYDEKGGKYKTELK
LNDFFIYKMPMKSMKINAFDTFEKNIFRVVVFLCVCLFIVNICFDINKERKINIENFL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             8580.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   NPHILKVVKNTEFYKNFIKDIKNLKNENHYTQYFNDDRKKLFFYNFVKNNLVETKYSC
GLLSVENVNYYKKQKNVKFSYLFGLSPQSEGFKGKGLYKNAPLYNKYENKQYGNPFHL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          /translation-"MKDFLSYAENNDLNIFKLYNSEEDCLKNLKYAIELKSEDFKNVN
SLELNDDILNIHENDKNSLLYNLHTNIINLKSSEFNINDLYKDVYTENEFENIKNLKI
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   /note="potential splice donor sequence may indicat further splicing of PFC0870W"
join(11431. .20416,20578. .20690)
/gene="PFC0875W, MAL3P7.4"
join(11431. .20416,20578. .20690)
/gene="PFC0875W, MAL3P7.4"
/note="PFC0875W (MAL3P7.4), hypothetical protein,
/note="PFC0875W (MAL3P7.4), hypothetical pr
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               1.1e-15, 53.2% shortened exon
                                                              SFFNTSGDFVFLLINCIIYLSIVFYKLLQIIPSKERTDKKNESEKTNYEEIILNNSYN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            PFC0870w"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           NGTQSYHNNNSTNSNDDQKKKNNNNNYYYYNNPDGLTTNVKYKTRVGDYALLNSNEK
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                YYPYYTLESDKKINEKNERNEKNERNEKNERNEKNEKNGKNEKNKDILSSTNNNVVMK
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     /product="hypothetical prot
/protein_id="CAB39024.2"
/db_xref="GI:8052275"
/db_xref="SPTREMBL:097278"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               /gene="PFC0870w, MAL3P7.3"
/note="revised splice donor sequence for exon
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 /product="putative elongation factor"
/protein_id="CAB39068.2"
/db_xref="GI:8052274"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             guanine nucleotide
VGVQRKKEQKKNRYTFFLKNFYLSNKEYKQPKENYEKNRNPFFYFIQKLFNLKRGNNV
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        /note="potential splice
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    codon_start=1/
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     /db_xref="SPTREMBL:097319"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    /codon_start=1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    . 8585
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          53.2% identity in 141 aa overlap, d exon 2, Pfam: match to PF00736 E nucleotide exchange domain Score 6
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   L protein, PFC0875w"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               may indicate
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61.10"
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at 5'
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REFERENCE
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 VERSION
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ACCESSION
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      DEFINITION
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                AC114238
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     KEYWORDS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ORGANISM
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Query Match
Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     156532 AAAAAAAAAAAGAACATATAATTTATTTAAATGTAAACTGAAGATAAAAATAAAATAAAA 156591
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 156652 ATATATAATAGAAAAAAATAAATTATAAAATTTTAATTATACATTATAAAATAAATTTA 156711
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         CE 1 (bases 1 to 165669)

RS Muzny, D. M., Adams, C., Adio-Oduola, B., Ali-osman, F.R., Allen, C., Anzardunge, H.C., Are, J.R., Ayele, M., Banks, T., Barbaria, J., Benton, J., Bimage, K., Blankenburg, K., Bonnin, D., Bouck, J., Benton, J., Bimage, K., Blankenburg, K., Bonnin, D., Bouck, J., Benton, J., Bimage, K., Blankenburg, K., Bonnin, D., Bouck, J., Benton, J., Brieva, M., Brown, E., Brown, M., Bryant, N.P., Bouck, J., Bowle, S., Brieva, M., Brown, E., Brown, M., Bryant, N.P., Burkert, C., Burrell, K.L., Byrd, N.C., Carron, T.F., Carter, M., Cavazos, S.R., Chacko, J., Chavez, D., Chen, G., Chen, R., Chen, Z., Chowdhry, I., Christopoulos, C., Cleveland, C.D., Cox, C., Coyle, M.D., Dathorne, S.R., David, R., Davila, M.L., Davis, C., Davy-Carroll, L., Diderich, D.A., Delaney, K.R., Delgado, O., Denn, A.L., Ding, Y., Dinh, H.H., Delaney, K.R., Delgado, O., Denn, A.L., Ding, Y., Dinh, H.H., Delaney, K.R., Delgado, O., Denn, A.L., Ding, Y., Dinh, H.H., Davis, C., Edgar, D., Edwards, C.C., Elhaj, C., Escotto, M., Falls, T., Ferraguto, D., Flagg, N., Ford, J., Foster, P., Frantz, P., Gablis, A., Gao, J., Garcia, A., Garner, T., Garza, N., Gill, R., Gariell, J.H., Gao, J., Garcia, A., Garner, T., Garza, N., Gill, R., Hartis, C., Harris, K., Hart, M., Havlak, P., Hawes, A., Hernandez, J., Hollandez, J., Johnson, R., Jollvey, S., Joudah, S., Karlsson, E., Kelly, S., Khan, U., King, L., Korvah, J., Kovar, C., Kartovic, J., Kureshi, A., Landry, N., Leal, B., Lewis, L.C., Lewis, L., Lozado, R.J., Lu, X., Lucler, R., Lunier, R., Lunier, R., Lunier, R., Martinez, E., Maheshwari, M., Martinez, P., Martindale, A., Martinez, E.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   63 TTAACAGAAACTTCCAAATTTTTTTTTTTTTATGGAACAAGAAATAACAGATAGAAAACTA 122
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    w
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             TTTGACTGTCCAGTTCGGTAATAATCT 389
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ACATATATATATATAATATATTATTAATTAAATAATTACGAAATTGAATATATACATA 156831
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 TTTTGTTGTGGAATGGAAGTAGTAATATACATTAAGCAAATTTTAAAAAATTATATAAGC 182
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             182;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Eukaryota; Metazoa; Chordata;
Mammalia; Eutheria; Rodentia;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Rattus norvegicus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            HTG; HTGS_PHASE1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                AC114238
AC114238.6 GI:21738343
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     165669 bp DNA linear Rattus norvegicus clone CH230-336N7, *** SEQUENCING AC114238
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Rattus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Norway rat.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      5.48;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Pred. No. 0.3;
0; Mismatches 205; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Score 59; DB 3; Length 253305; Pred. No. 0.3;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Craniata; Vertebrata; Euteleostomi;
Sciurognathi; Muridae; Murinae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        IN PROGRESS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               HTG 13-JUL-2002
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JOURNAL
REFERENCE
AUTHORS
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as soon as it is available and be preserved.

the accession number will

1074:

3401 4593

4693

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gap of unknown contig of 1779 gap of unknown contig of 1512 gap of unknown

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1075 1175 2180 2280 3301

1074: contig of 1074 bp in length
1174: gap of unknown length
2179: contig of 1005 bp in length
2279: gap of unknown length
3300: contig of 1021 bp in length

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Miner, Z., Mitchell, T., McLeod, M. P., Meador, M., Mei, G., Metzker, M., Miner, Z., Mitchell, T., Mohabbat, K., Morgan, M., Morris, S., Moser, M., Neal, D., Newtson, J., Newtson, N., Nguyen, A., Nguyen, N., Nickerson, E., Newtson, N., Nguyen, A., Nguyen, N., Oragunye, N., Oviedo, R., Pace, A., Payton, B., Peery, J., Perez, L., Pickens, R., Primus, E., Pu, L. L., Quilles, M., Ren, Y., Rives, M., Rojas, A., Rojubokan, T., Rolfe, M., Ruiz, S., Savery, G., Scherer, S., Scott, G., Shen, H., Shooshtari, N., Sisson, I., Sodergren, E., Sonaike, T., Sparks, A., Stanley, H., Stone, H., Sutton, A., Svatek, A., Tabor, P., Tamerisa, A., Tamerisa, K., Tang, H., Tansey, J., Taylor, C., Taylor, T., Telfrod, B., Thomas, N., Thomas, S., Ward-Moore, S., Warren, R., Washington, C., Watlington, S., Williams, G., Williamson, A., Wleczyk, R., Wooden, S., Worley, K., Weinstock, G. and Gibbs, R.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Direct Submission

Direct Submission

Direct Submission

Submitted (13-JUL-2002) Human Genome Sequencing Center, Department of Molecular and Human Genetics, Baylor College of Medicine, One Baylor Plaza, Houston, TX 77030, USA

Baylor Plaza, Houston, TX 77030, USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Submitted (07-MAR-2002) Human Genome Sequencing Center, Department of Molecular and Human Genetics, Baylor College of Medicine, One Baylor Plaza, Houston, TX 77030, USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Worley, K.C.
NOTE: Estimated insert size may differ from sequence length (see http://www.hgsc.bcm.tmc.edu/docs/Genbank_draft_data.html).

NOTE: This is a 'working draft' sequence. It currently consists of 49 contigs. The true order of the pieces is not known and their order in this sequence record is arbitrary. Gaps between the contigs are represented as runs of N, but the exact sizes of the gaps are unknown.

This record will be updated with the finished sequence.
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                                                                                                                                                                                                                                                                                                                                   Sequencing vector: Plasmid;
Chemistry: Dye-terminator Big Dye: 100% of
Assembly program: Phrap; version 0.990329
Consensus quality: 128160 bases at least (
Consensus quality: 133217 bases at least (
Consensus quality: 136246 bases at least (
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Center clone name: CH230-336N7
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Contact: hgsc-help@bcm.tmc.edu
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Best Local Similarity
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1697 AAAAATAATTTTAATAATAATT 1720
                                                                          TTAATAATGCATGGTGCGATT--CAGAATTGGGACAACAATGAAAACGGAATTAAAATAT 277
                                                                                                                                                                       AAGAAATAACAGATAGAAAACTATTTTGTTGTGGAATGGAAGTAGTAATATACATTAAGC 159
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                                                                                                                                                                                                                                                                                                                                                                            /organism="Rattus norvegicus"
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1. .165669
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132057: contig of 7534 bp in length
132157: gap of unknown length
139108: contig of 6951 bp in length
139208: gap of unknown length
149265: contig of 9957 bp in length
149265: gap of unknown length
165669: contig of 16404 bp in length.
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DEFINITION
Direct Submission
Submitted (25-AUG-1999) Multimegabase Sequencing of Washington, PO BOX 357730, Seattle, WA 98195,
                                                                                Rowen, L., Madan, A., Qin, S., Abbasi, N., Baradarani, L., Birditt, B., Bloom, S., Dors, M., Dickhoff, R., Harrison, G., James, R., Lasky, S., Madan, A., Ratcliffe, A., Shaffer, T. and Hood, L.
                                                                                                                                                                                                             Direct Submission
Submitted (30-MAR-1999) Multimegabase Sequencing of Washington, PO BOX 357730, Seattle, WA 98195,
                                                                                                                                                                                                                                                                                                   Young, J., Rowen, L., Madan, A., Qin, S., Abbasi, N., Dors, M., Dickhoff, R., James, R., Loretz, C., Lasky, S., Madan, A., Prescott, S., Ratcliffe, A., Shaffer, T. and Hood, L.
                                                                                                                                                                                                                                                                                                                                                                                                                                                     Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalla; Eutherla; Primates; Catarrhini; Hominidae; Homo.

1 (bases 1 to 192389)

Rowen,L., Madan,A., Qin,S., Abbasi,N., Baradarani,L., Birditt,B., Bloom,S., Dors,M., Dickhoff,R., Harrison,G., James,R., Lasky,S., Madan,A., Ratcliffe,A., Shaffer, and Hood,L.

Sequencing of human chromosome 14
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AC007182
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507E23 map 14q24.3, complete
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FEATURES
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                                                                                                                     /note="low quality data"
/note="low quality data"
complement(join(163771. .163850,163987. .164105,
167102. .167192,169586. .169663,172991. .173087))
/note="This gene, predicted by Genscan, is confirmed
several ESTs. See, for example, W27204, AA504716. T
nearest BLASTX similarity is to hypothetical proteins
s. pombe and S. cerevisiae."
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       /note="Intron-exon boundaries were defined partly by Genscan and partly by ESTs. See T79253 and AA305338. closest BLASTX hit is to AF118637, 'C receptor.'"
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QRQTQKaDTLHLESEDLEKQNAALRKEIKQLTEELKYFTSVLNSHEPLCSVLAASTPS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             and
    /translation="maQVDSGLELSWGSLFAAAAAAATAVLGARSPAMGNTLQSFRDH
TFLYEKLYTGKPNLVNGLQARTFGIWTLLSSVIRCLCAIDIHNKTLYHITLWTFLLAL
                                      /product="unknown"
/protein_id="AAD51373.1"
/db_xref="GI:5764707"
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                                                                                                                                                                                                                                                                                                                                 may be a processed pseudogene
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/gene="RPS24a-like"
/note="Similar to RPS24a. Since there
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KYPPSRAQSLSYALTSPDASYLGSIARLFKNLNFVLLVITYGLNAGAFYALSTLLNRM
VIWHYPGEEVNAGRIGLTIVIAGMLGAVISGIWLDRSKTYKETTLVVYIMTLVGMVVY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              /translation="MVNEGPNQEESDDTPVPESALQADPSVSVHPSVSVHPSVSINPS
VSVHPSSSAHPSALAQPSGLAHPSSSGPEDLSVIKVSRRRWAVVLVFSCYSMCNSFQW
IQYGSINNIEMHFYGVSAFAIDWLSMCYMLTYIPLLLPVAWLLEKFGLRTIALTGSAL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  /note="low quality data"
join(91189. .91857,134295. .134436,136828. .136968,
145845. .145912,147126. .147229,151568. .151678,
153171. .153276,153398. .153509,154059. .154114,
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join(34899. .34961,37300. .37404,58678. .58887)
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and 368K8, Accession AC009399."
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/clone_lib="RPCI-11"
                                                                                                                                                                                                                                                                                                                  126360
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           NCLGAWVKLGSLKPHLFPVTVVGQLICSVAQVFILGMPSRIASVWFGANEVSTACSVA
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/db_xref="GI:5764708"
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/db_xref="GI:5764706"
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Location/Qualifiers
                                                                                                      /codon_start=1
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Agency: Deutsche Forschungsgemeinschaft (DFG).
* NOTE: This is a 'working draft' sequence.
* This sequence will be replaced
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97 AACAAGAAATAACAGATAGAAAACTATTTTGTTGTTGGAATGGAAGTAGTAATATACATTA 156
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ATGTATGTGAAATTACTTTGTAAGTGCTATACAAATGTAAGGCATTATTTTTACTGGTTT 176758
                         Submitted (18-MAY-2002) Genome Analysis, Institute of Molecular Biotechnology, Beutenberstr. 11, Jena 07745, Germany CDS predictions from GeneID may contain errors. Further Information is available from IMB Jena, Department of Genome Analysis (http://genome.imb-jena.de/dictyostelium/) and the Univerity Colonge, Institute for Biochemistry I
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Dictyostelium discoideum
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Dictyostelium discoideum chromosome 2 ma
AX4, *** SEQUENCING IN PROGRESS ***, in
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Gloeckner,G., Eichinger,L., Szafranski,K., Pachebat,J., Dear,P., Lehmann,R., Baumgart,C., Parra,G., April,J.F., Guigo,R., Kumpf,K Tunggai,B., Cox,E., Quail,M.A., Platzer,M., Rosenthal,A. and
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//www.uni-koeln.de/dictyostelium/project.shtml
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191730. .191800
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173850. .173930
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163815. .164050
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             CKFKIFLKNRKONKKLKKORKKOKQEDEYEEDEEDKEEEVENNYLFNFKNRKNEIKLK
IKNNFWYLISIIFCKWRFTIKFTILLSIFSIGYYEILTRSYFILEQNSSGFVYTFLYV
ASPSYGASGFYCCMRFFGTLLOVFSAYVYGVLFSLADSDGTKGLAYIALTTTLYFSIL
FFVRGKPIQSFGNFFILSYATITFPEYTQDHALIITTLLRAFHISLAVFVIMLSSILI
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EIDLNKINYKKSLNYSQERILKYFKRIEKVEMEMCKEYSKIEITNDLLHLEEDSQCEI
SRIHFFVNLLTSFTKQQKELSTIVYTMSRCLYRQNRIYHFEMFLLILCWFLNFPKFLY
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KECDQEFWNKDLVSHFNQLAILLEKNHNMINSMQISIDKDISNPSCHFLLPLIPFINI
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               /product="hypothetical protein"
/protein_id="AAM33148.1"
/db_xref="GI:20976559"
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/note="ORF_ID:dd_03233"
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GLTLSLEQELAPFNIKVVLLSPGGFRTIITNKEKFKLVENPIPEYYPNSTPQNSLEAF
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EKSENNNEKINQMKSILNCTL"
                                       /product="putative splicing factor"
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/db_xref="GI:20976560"
                                                                                                                                                                                                                                                                                              NMSTLNRVSNCLNIPMN"
                                                                                                                                                                                                                                                                                                                                          SNSSINSSKNINNNNNSTCIDSSTFTSSSSDNNSEDLIIPINRSQFIRHTSIGGTEYN
                                                                                                                                                                                                                                                                                                                                                                                  FCVHQLGCLIYTFDLFINLMSNITKY IWSITKTILIERKDSNYLYNNNLNSLDNLVTM
                                                                                                                                                                                                                                                                                                                                                                                                                                                                          VGSEF1IDNCQEDGNDSYHNHHHHHHHNSKNYDQTNFLLDVKSLLLPKFNYLIKELDE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    EFKISPKRKSHKKIIKNIHSRLSNSLSNLPNLSQINNNNNNSISLSNYEIEINNNNNK
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     /product="3-OXOACYL-(ACYL-CARRIER PROTEIN) REDUCTASE
1.1.1.100). 6/101"
translation-"MENKRKQKDEIVLVNGSNDTTPNKKQKNELQVVSSGGGREIILG/
                                                                                                                                                                                                          join(10546. .10804,10924.
/note="ORF_ID:dd_02343"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              PKETFQETMRPTFLETRSLITNQRSLMFNSRFELLFNKQKYKDLKSLLNNTSSEYMVL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          LPYYDHRELEINLLDISIKQLEAFKSIFNHNSHWFDINNNRNIDDLTSISTVSSMIMI
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/note="ORF_ID:dd_02345"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 /organism="Dictyostelium
/strain="AX4"
                                                                                                                                                                       codon_start=1
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         /db_xref="taxon:44689"
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                                                                                                              /translation-"MSAQRQFSEDLWDKFESVVKKVDNGKIFTQQLSKFLSKQQQIES
AYAKSIVKLCKDKSFAÞEVEMGTLRDSFQCYREQLELIGALHEFSNRLEKLYTIGIB
GYLESERKQRKALIANGEKCTKDLKTÄDESNESKAKQNYEKLKKKQEBANEDLSKQPPG
AKEQKARKTLESATKAADKGDNEYRESVKCLQQNQQKFYHEEMFRILDDLQRFEVERI
DKSKOMLMEVITQNELYPPAVIIHNENIKKGIESIDRERDLQNIILVTMSGAQKPPEA
QYEPYQSGGFAIVNSSSNSILNISKSGELNGGGSIQNGASIISSPQQPQYQNIDHQ
TPPQPNIIQOHQQSNNNNNTNNNSKYMTTPPEPQPQDQQQLPQPTQLNNPPQPPIS
LSKNDSSNSINSNSNGEIVRALYDYNATEENEISFKANALIKYVLRDESGWWQGMVIG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                VEIQFENSKKINSLKKKKNFRFQIPNSPQ"
complement(22366. .23967)
/note="ORF_ID:dd_01650"
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/db_xref="GI:20976602"
/dr. The first of the f
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VKTIRKETGGTVKLQLMDTAGQEFKSJTQTFYRGSHGVIVVDDVTDPKSFERCKNW
VEDINQYTQDKIILLVGNKSDWADQKVTFEGGGDEMAEQLKTKFLEVSAKENNGVTQ
VFDLLVQDIEATMKNSKVAQNQLNLNSEVGGKRGCC"
join(15211...15350,15458...16451)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        /translation="munnpiiknykkslsqsfddllvnkdiddsftcpiclkllidar
OGCSEGHVFCNNCITSWLKNKNNCAVCRLHISQNCLSKNRFLESNIKKIKVFCPNKND
LNDLNDDSDGCPEILEIGNVESHSLKCIHRFVLCQYGGDKCGFVRLNKLLSHEIECPF
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               complement(join(21183. .21470,21613. .21894))
/note="ORF_ID:dd_01649"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               GDDKDQLFVIIDFSEDILKLYYEEPKVEKEKEKEKEKEESQSFIGKYWFYLLPLFLII
LYNMAAPPPAAQTNAAASQGAGSRNNNNNN"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  /translation="MKFNKITIISIVIALFTIILQISESITVSNLNNQKDIEFTMYHN
EDQSKSCKILFKPKLIPHSTNSITSVDSINFKKAIQIKCKNSLTKESRSLYQKSCDLF
KTTVVSDKDPSNLSFSSLPKGNLNDSSLQYEFLKINLDSNNMNIVASNYQLKKSPPVT
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AGILLYIGFSLMIKDFPEDMEELCRGKKYEYFLRAGLFIGLWVGAAMMAFIGKYL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   complement(join(17012. .17403,17496. .18273))
/note="ORF_ID:dd_01647"
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GHKGTILEHMSTDSNEIYTAGYDKSIGVADDSNKGELIKRIREBGVVNSCCEARRGP
PLVASGSDBASARIFDTRSKGSTHLFOHKYPYTSVCFSDASDOLITGGIDNVIRVADI
RNQEDPLYTLAGHQDTITSTSVSKDGAYLLSNSMDNSCKIWDIRPYAPPNRNIKTFNG
                                       DEGWFFGSNESNVSARFPSNYVQVI"
                                                                               ESDRIGVFPSNFISDSSDSSKKRVDVAGRKCKVLYDYRTDCEGELNIKEGEILTIEYE
                                                                                                                                                                                                                                                                                                                                                                                                                                                             /product="Sequence 3 from Patent W00075321. 6/101"
/protein_id="AAM33153.1"
/db_xref="GI:20976564"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            /product="hypothetical protein"
/protein_id="AAM33152.1"
/db_xref="GI:20976563"
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/protein_id="AAM33151.1"
/db_xref="GI:20976562"
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/protein_id="AAM33150.1"
/db_xref="GI:20976561"
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/codon_start=1
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26525,26681.
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REMARK
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Submitted (21 MAR-2002) Genome Analysis, Institute of Molecular Biotechnology, Beutenberstr. 11, Jena 07745, Germany CDS predictions from GeneID may contain errors. Further Information is available from IMB Jena, Department of Genome Analysis (http://genome.imb-jena.de/dictyostelium/)
                                                                                                                                                                                                                                                                                                                                                                Eukaryota; Nycetozoa; Dictyostelida; Dictyostelium.

1 (bases 1 to 27291)

Gloeckner,G., Eichinger,L., Szafranski,K., Pachebat,J., Dear,P.,
Lehmann,R., Baumgart,C., Parra,G., April,J.F., Guigo,R., Kumpf,K
Tunggal,B., Cox,E., Quail,M.A., Platzer,M., Rosenthal,A. and
                              (http://www.uni-koeln.de/dictyostelium/project.shtml
                                                                                                                                                                                                                Direct Submission
                                                                                                                                                                                                                                                                                        The
                                                                                                                                                                                                                                                                                                                       Sequence and Analysis of Chromosome 2 of Dictyostelium
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Dictyostelium discoideum.
Dictyostelium discoideum
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Dictyostelium discoideum chromosome
                                                                                                                                                                                                                                                                                                                    Unpublished
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              AC115575.1 GI:19569867
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                AC115575
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                                                             the Univerity Colonge,
                                                                                                                                                                                                                                               Dictyostelium Genome Sequencing Consortium (bases 1 to 27291)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            HTGS_PHASE2.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 SEQUENCING
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     LFMHNMLIRÞANREELRNFGEÞDYTTYNAGQFÞANRYTKGMSSSSSIAIDFARKEMVI
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DINRELIGDDEHVMTDTGCFNIEGGCYAKCIDLSREKEÞEIFDAIKFGAVLENVVYNE
YSRKVDYNDVSITENTRCAYÞLEHIÞNAKFÞAIAGHÞKNIIMLTCDAFGILÞÞVSRLD
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 /product="sequence 3 from Patent W00075321. 6/101"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        GVPSEILMPINGWADKEKYVSTMHKLAKLFIENFKKFQDKASPELVAAGPILPQ"

join(28999. 29084, 29176. 29317, 29453. 30610)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ANQVMYHFIQGYTAKVAGTEVGVTEPTATFSSCYGEPFIVWHPTKYAEMLASQLHKHS
ARAWLINTGWTGGSHGVGSRIKLAYTRAIIDAIHSGELEKIPTTKMDVFGFQVPNSCP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         /note="ORF_ID:dd_00794"
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/codon_start=1
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Pred. No.
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                                                   Institute for Biochemistry I
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2 map 1180800-1208089 strain
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         gency: Deutsche Forschungsgemeinschaft (DFG).

MOTE: This is a 'working draft' sequence.

This sequence will be replaced

by the finished sequence as soon as it is available and

the accession number will be preserved.
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SQPYEKNVGFIDSVWLSSKNIRSDDFGLIGQGTIKNOVISISNSFIYLPDPPIKCPEL
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IYPFQENVGKYFDNNWLNYKSVIQDHSKLIALGTINNNNEMVVSNAYINIPDPIEKCI
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          complement(join(2838. .3347,3546. /note="ORF_ID:dd_00013"
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N"
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/chromosome="2"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              /strain="AX4
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SLIEDETTENELRSHYNLLFQPDHFKDVVAERSASKCENFCSKPLGVKKLNQKYFI
SVKEQKVYNVEELSHFCSSDCLVKSKLYASTLDETAVYLTVESKKILPEQTILISQ
TKTOSQTQTQSQQAPKPASKPIEFLNKFEKSLVITENENASLIPPNLTFDKNVDNEKT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         FANTEVTIDJOGERSETGTMVLKLGY LEVVEPDKRNDK LIPTYOKGERETPKRIDLT
KGTTVAPHY ITEAELLTAMDNIK IGTDATMATH IQTIQDRYYKK NESKOFVPSNLGV
SLVASYELMGE EFSKRUKLRAA IEADVDK ISRGOKTKOEVLLST IEKYKQLYQLANONI
NCFDRSFREYYEPADPKGGEFRVLVSQFSRCGKCNGKMQYK SDQNPEAPKRILECPQC
IDTFDLPKNGDISQLVTSMGVPQNCP IQQYQVLSYRNEINDKSYTICPKCRUSPEDPI
HKKPEPHCFQCTENCNLATGNKOOQOQQOQOQOQOTNYNRNNNNNNTNSARPITTRTTRT
TTQHRTFTASNNNENNNNRNSDRNNNNPIF
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         /translation="MLKNTFITLIFTIISISICFGSQLPTNYYEKVTHVPIYCITTPC
SQYRVYKVNTQDPEIVIENTVFPNGVEQNYESLQEANTAILYCII IANRNGYNVNDFK
VKRVKVLTGVBEIVIENTVFPNGVEQNYESLQEANTAILXIDNAATNVNDVKQP
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LKQQGHYTVYERDSNRCLTNPQCSNDNDTRACILSIPTCSTGYDLVSYTSISTCPAY
                                                                                                                 EELFKPHISNYHMYYSTLSQFTTKHTNNFLQFNQINYEYILEQNLQIKSNLHSQLSLV
YQSVIDQLGFKITTAKEKVTILIDTFKFDKPVPSLRRNHWKILSSIDEEILKDIKDNN
DKFENLVKECNFDMETLKVFQDLLIQGYQ"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              complement(join(16447. .16585,16689. .17423,17492.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    SRLINNNQFVYPKSGKNNDNSHPPIHPTSSATGLSGNLKKIYDFITRRFLACCSEESV
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KMIPVTFSWCRNRLFDYTAAFILYEKCLDNTEATVVDVTSKESRYRPVPLTTIELQKA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  NILNFNDCEMTFTSVTGHLMEIDVVEQFKPWASCDPIQLFDAPIRKTVPSDKEPLKKT
LEREIKKADILILWLDCDREGENIAFEVLEVCKNAKKKFEFYRAHFSAIIPREIDRAC
KNLAKPNEKDSIAVDTRMEIDLRIGAAFTRFQTLYLKKFKIISNSDNQPKTTTPANGN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         complement(join(13472. .15871,15996. .16082))
/note="ORF_ID:dd_00009"
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join(12238. .12622,12711. .13189)
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SCLKLLQDNNIKTIFNLDNNQLFNIQQVTNSSVILNSITSNITKNSSSSGGSIFGNCN
LNILFEKQSEYYIEIKNNNCKICTFLLKAPSIFIIEEVQRSLNDSISILSLIVKSKKF
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                                                                                                                                                                                                          EDDTLLGDEQDDAPMVLNEDEDENDNNINEDEEDENKSDKSEDEFSLFRPTQMSSKRV
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10316...10739,10891...11140))
/note="Oker_Dicad_00019"
/codon_start=1
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KEYWORDS
SOURCE
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                                                                                                              REFERENCE
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Best Local
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     GTATACAATTATTGAATAATTGGAATTTACAATATTTTATAAAATACCAATTGAATTATT 7481
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              GTGGAATGGAAGTAGTAATACATTAAGCAAATTTTAAAAAATTATAAGCCTATACG 189
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ATTTTGGGTGATTTTTTAAATTTGTAGATTGTACCAAATTAGGTAAATTATTGGGCTATT 7541
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        AAAAACTGAATATTTTTATTATCATTGAAGTAATTCTGATATCTATTGTTATAATTTAAT 7601
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   161;
                     1 (bases 1 to 169546)
Hyman, R.W., Fung, E.L., Qin, F., Rowley, D.,
Kurdi, O.B., Conway, A.B. and Davis, R.W.
Plasmodium falciparum 3D7 chromosome 12
                                                                                                                                          Plasmodium falciparum.
Plasmodium falciparum
Eukaryota; Alveolata;
                                                                                                                                                                                                                                                                                                                                                    ACO04157 169546 bp I
Plasmodium falciparum chromosome 12
Unpublished
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ITGLAGVTLFAPHDAIHYIQLLHTQYPALVYPAKFAVALPLTYHECTGVRHIIMDETV
KGLSISQIESSGKVLLAVVAVLSTIFTEVSEK"
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RALYDMRNNVESTINHEMRELOGGYBERGORLDEEDRLAGREEDEYERRERNK
KRVNDLLLEIKYSSPEKOKOLAOSK.EGODVLKDEDHLTVFDQPEPOLTTIYYPVPQ
IPOPRYVNNEPTTFTMPSFSPPDYNSSMENNGNKPPTTTTTTSNQPFQNLDPENNTA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               /note="ORF_ID:dd_00016"
/codon **---
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              translation="MKMDAFSCFGVRNKKKSVLLKQMQAEEKEAQLNRNYFNLLSTEL/
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     IQNLLDITIKVENSKNASN"
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                                                                                                                                          Apicomplexa; Haemosporida; Plasmodium
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Indels

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7661

linear 3D7, \*\*\*

HTG 12-AUG-2000 SEQUENCING IN

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REFERENCE
AUTHORS
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Search completed: March 30, Job time: 12061.1 secs
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ORIGIN
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                                                                                                                                                                                                                                                         13160 CTTACATACTTTATTATATTAAATACAAGGAATGTTTTAATGGATATAATAGAATTGATT 13101
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                                                                                                             312 GTTTTCTGACTATTGAGGGGCAAAAAAAAAAAGACAATGCCAAAAGTCTA 358
                                                                                                                                                                                                             192 CTCAAAGTATGTTATCTAGTAGGTGTAATTAATAATGCATGGTGCGATTCAGAATTGGGA 251
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                                                                                                                                                                                                                                                                                                                                                                                                                                                           TTCCAAATTTTTTTTTTTTTTATGGAACAAGAAATAACAGATAGAAAACTATTTTGTTGTGG 133
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On Aug 12, 2000 this sequence version replaced gi:8810447.
* NOTE: This is a 'working draft' sequence. It currently
* consists of 2 contigs. The true order of the pieces
* is not known and their order in this sequence record is
* arbitrary. Gaps between the contigs are represented as
* runs of N, but the exact sizes of the gaps are unknown.
* This record will be updated with the finished sequence
* as soon as it is available and the accession number will
* be preserved.
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Submitted (19-FEB-1998) Stanford DNA Sequencing and Technology Center, Stanford University, 855 California Avenue, Palo Alto,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  2 (bases 1 to 169546)
Hyman,R.W., Qin,F., Fung,E.L., Conway,A.B. and Davis,R.W.
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/clone="3D7"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             /organism="Plasmodium falciparum"
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23666: gap of unknown length
169546: contig of 145880 bp in length.
                    2003, 07:31:25
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Maximum Match 100%
Listing first 45 summaries
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length: 2000000000
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Gapop 10.0 , Gapext 1.0
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1101
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1: /SIDS2/gcgdata/
2: /SIDS2/gcgdata/
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                                                                                                                                                                                                                                                                                                                                                                                                                                                      /SIDS2/gcgdata/geneseq/geneseqn-emb1/NA1980.DAT:*
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

## SUMMARIES

Result No.	Score	Query Match Length DB	Length		ID	Description	
۳	1101	100.0	6888	21	AAA59599	DNA encoding a cyt	
c 2	56.6	5.1	6107	24	ABL70390	Chemically treated	
c u	56.6	5.1	6107	24	AAS61342	Human gene regulat	
c 4	56.6	5.1	6107	24	ABK31431	Signal transductio	
5	54.2	4.9	875	21	AAA01920	Human colon cancer	
c 6	54.2	4.9	6113	24	ABL32803	Human immune syste	
c 7	53.8	4.9	37973	24	ABL34197	Human immune syste	
æ	53.8	4.9	83391	24	ABQ67094	Human angiogenesis	
c 9	53.4	4.9	17131	24	ABL33053	Human immune syste	,

45	C 44	c 43													30	29		c 27	26						c 20		18		c 16		14	13	12	11	10
50.4	50.4		0		0		0	.0		51	51	۳		51.2		_	۲	۲.	52	52	52	52	52	Ñ	52.2	Ñ	Ñ	Ñ	Ñ	Ñ	53	53	53	53	53.2
4.6	4.	4.6			•	٠	•		•	٠		4.7	4.7	4.7	4.7	4.7	4.7	4.7	4.7	4.7	4.7	4.7	4.7	4.7	٠					•	٠		4.8	4.8	4.8
. 8085	5689	5689	5689	12405	12405	12405	6254	5880	5880	10286	10286	23695	5690	5690	3738	4041	47108	641	7459	6636	5309	5309	5309	78925	7746	7746	5940	4501	16228	16228	72049	66933	57273	54108	8170
N	24																									24	21	24	24	24	22	22	24	24	24
AAS46479	ABK28226	AAS46426	AAS45384	ABK28169	AAS61143	AAS45330	ABL33621	ABK28177	AAS46331	ABK28148	AAS45309	ABQ66981	ABK28205	AAS45368	AAA70178	AAA70170	ABK31511	ABQ56694	ABK31382	ABN80023	ABL33736	ABK40039	AAS46527	AAC89888	ABL33856	ABK40047	AAA70105	ABK33968	AAS61424	ABL70459	ABA82623	ABA82625	278	27	ABK28257
Tumour suppressor	DNA transcription		Chemically pretrea	~	Human gene regulat	Chemically pretrea	Human immune syste	DNA transcription	Tumour suppressor	DNA transcription	Chemically pretrea	Human angiogenesis	DNA transcription	Chemically pretrea	Plasmodium falcipa	Plasmodium falcipa	Signal transductio	Human colon cancer	$\mathbf{L}$	_	Human immune syste	hemical	Tumour suppressor	Ξ.		Human chemically p	Plasmodium falcipa	Human DNA for stag		call	HBM gene	HBM o	high bone	an high bōn	DNA transcription

## ALIGNMENTS

DNA encoding a cytochrome P450 enzyme designated DWF4.

DWF4; cytochrome P450 enzyme; brassinosteroid; 22alpha-hydroxylation; plant phenotype; cell elongation; ss.

## Arabidopsis sp.

FT	FT	Į.	F	ΕŢ	ΡŢ	FΤ	ΕŢ	FT	Ŧ	Ŧ	ΕT	ΕŢ	FΤ	ΗT	ŦΤ	HÆ	X	S	X	X	XW	×	DE	<b>4</b> 5	3;	ž	A X	Ħ	AAA5	
	intron		exon		intron		exon				CDS		TATA_signal		promoter	Key		Arabidopsis sp.			DWF4; cytochrome	,	DNA encoding a cytochrome		14-NOV-2000 /fi		AAA59599:	AAA59599 standard;	AAA59599	
/*tag= g	9	/*taq= f	8	/*tag= e	3424 3503	/*tag= d	3423	/note= "contains introns"	/product= "DWF4"	/*tag= c	32036110	/*tag= b	30603125	/*tag= a	13203	Location/Qualifiers				cell	P450	,	ytochrome P450 enzyme designated	tac cuct)	(first optro)			d; DNA; 6888 BP.		

intron

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exon

3914..4066 /\*tag= h 4067..4164

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Best Local :
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11-FEB-1999;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              intron
                                                                                                                                                                     The present sequence encodes a DWF4 polypeptide. The polypeptide is a cytochrome P450 enzyme that mediates multiple steps in synthesis of cytochrome P450 enzyme that mediates multiple steps in synthesis of present of the present organs, plants display a dramatic reduction in the length of different organs, plants display a dramatic reduction in the length of different organs, and this size reduction is attributable to a defect in cell elongation. The DWF4 polypucleotides and polypeptides can be used in diagnostic assays and to generate antibodies, which can be used to produce
                                                                                                                                                                                                                                                                                 New isolated \text{dwf4} polynucleotide useful for altering the phenotype of plants, for diagnostic assays and in the production of antibodies -
                                                                                                                                                                                                                                                                                                                                                          (ARIZ-) ARIZONA BOARD OF REGENTS
                                                                                                                                                                                                                                                                                                               P-PSDB; AAB07921
                                                                                                                                                                                                                                                                                                                                           Azpiroz R, Choe S,
                                                                                                                                                                                                                                                                  Claim 3; Fig 10A-G;
                                                                  2102
                                                                                                                                          Sequence 6888 BP; 2294 A; 1010 C; 1193 G;
                             2162
                                                                                                                                                            lmmunogenic compositions.
           121
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                                                                Local Similarity
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100.0%;
milarity 100.0%;
Conservative 0;
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99US-0119658
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                                                                                                         Score 1101; DB 21;
pred. No. 1.6e-208;
); Mismatches 0;
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                                                                                                                                                  0 other;
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                                                                                                                               Length 6888;
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RESULT 2
ABL70390/
ID ABL7
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AC ABL7
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ABL70390;

ABL70390 standard; DNA; 6107

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                                                                                                                                                                                                                 GGTTTGACTGTCCAGTTCGGTAATAATCTAATAACTCTGTCTTTGACCGCACGCTCGTGT
                                                                                                                                                                                                                     ATCCTAAGGGTAATTTTGGAAATCCCAATTTAAACCGATTGAGACCGTACCGGACTTCCT
                                                                                                                                                                                AGGGGTCCTTCTGACATTTTCACTGTTCTACCCCTACTCGTGAGCCCACCCTTTTCCCAT
                                                                                                                CARTTGATTATAGATATATCCATTAATCCATGATATTTATGATATAAATAGCTGTTAAAC
                                                AGTATTAAAAGGAGCATAACGAGGCAACAAAAGTAATGAACACGGAGAAAACCAAT
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                    AGAGAGAGAAACTAGCTCC
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           CC The invention relates to a nucleic acid comprising a sequence of at least CC 18 bases of a segment of chemically pretreated DNA of genes associated CC with cell signalling. The activity of the modified sequences of the CC invention may be described as cytostatic. The object of the invention is comproved the chemically modified DNA of genes associated with cell control of the chemically modified DNA of genes associated with cell control of the contro
                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Matches 164;
                                                                                                                                                                                                      4651
                                                                                                                                                                                                                                                                                              4711
                                                                                                                                                                                                                                                                                                                                                                                         4771
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Sequence 6107 BP; 1604 A; 136 C; 1251 G; 3116 T; 0 other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Nucleic acid, useful for diagnosis and therapy of diseases associated with cell signalling e.g. cancer, comprises chemically modified genomic sequences of genes associated with cell signalling
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Claim 1; SEQ ID NO 280; 24pp+sequence listing; English.
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01-SEP-2000;
                                                                                                                                                                                                                                                                                                                                             86
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cancer; tumour;
                                                                                                                                                                                                                                                                                                                                                                                                (EPIG~) EPIGENOMICS AG.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            10-JAN-2002
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Chemically treated cell signalling DNA sequence complementary to#140.
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TAAAACTCATAATTTAAAAAAAAATAACGAAAACTACTTATTATTATCACTTTTCCTTTTCC
                                         GAATTAAAATATTAACTTTAAAATAAATAAATTTGAGTAAATGTGTTTTCTGACTATT
                                                                                     TAAAATAAAAAAATAATTAATTCATATATCATAACAAAATTACTAATACTATCTAAAAT 4532
                                                                                                                       TCTAGTAGGTGTAATTAATAATGCATGGTGCGATTCAGAATTGGGACAACAATGAAAACG
                                                                                                                                                                             AAACTTAACTATATAAAACTCATATAACTAAAAAAACGTAAAAAATAAACTAAAATAAAA
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                                                                                                                                                                                                                                                                                                                                                                CAAAAAAATAAAATAAATAATAATAATAAAAAAATCTAAAAATACATAAAATATCCTT 4712
                                                                                                                                                                                                                         AATATACATTAAGCAAATTTTAAAAAATTATATAAGCCTATACGCGCTCAAAGTATGTTA
                                                                                                                                                                                                                                                                                                                    TTTTTTATGGAACAAGAAATAACAGATAGAAAACTATTTTGTTGTGGAATGGAAGTAGT 145
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                     5.1%;
nilarity 47.8%;
Conservative
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2000DE-1043826.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                0; Mismatches 179; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Score 56.6; DB Pred. No. 0.044;
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The invention relates to 224 nucleic acid sequences comprising at least CC 18 bases of a chemically pretreated gene associated with gene regulation consists of a chemical pretreatment converts cytosine bases unmethylated at the CC 5-position to uracil or another base with hybridisation behaviour CC dissimilar to cytosine, to enable analysis of cytosine methylations. CC useful in the diagnosis of diseases (or predisposition to diseases) CC associated with gene regulation and in therapy of such diseases) CC enabling analysis of the cytosine methylation patterns of such genes, CC disorders, haemophilia, solid tumours and cancer, Werner syndrome, CC asthma, HDR syndrome, Saethre-Chotzen syndrome, renal disease, cardiac CC asthma, HDR syndrome, Saethre-Chotzen syndrome, renal disease, correctangesia, graft versus-host disease. The present sequence is a cc associated with the human gene regulation associated genes. CC sequence included in the sequence data for this specification and is concern the sequence data for this patent did not form part cc format directly from MIPO at cc format directly from WIPO at cc format directly from WIPO at cc.
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AAS61342/c
ID AAS613
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                     ftp.wipo.int/pub/published_pct_sequences
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07-APR-2000;
30-JUN-2000;
01-SEP-2000;
                                                                                                                                                                                                                                                                                                                                                                                                                                           New nucleic acid sequences from chemically modified genes associated with gene regulation, useful for analysing cytosine methylations for diagnosis and therapy of diseases e.g. severe combined immunodeficiency
                                                                                                                                                                                                                                                                                                                                                                                                         Disclosure; SEQ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             WPI; 2002-017470/02.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Human; Gene regulation-associated gene; severe combined immunodeficiency; cardiac damage; inflammatory response; Haemophilia; Werner syndrome; asthma; HDR syndrome; congenital heart defect; Saethre-Chotzen syndrome; renal disease; Preclampsia; cardiac allograft vascular disease; colorectal cancer; thyroid cancer; oesophageal cancer; ds; tumour; immunostimulant; cardiant; antiinflammatory; coagulant; antiasthmatic;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             (EPIG-) EPIGENOMICS AG
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                gene regulation-associated gene oligonucleotide #297.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Piepenbrock C,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ; 2000DE-1019058.
; 2000DE-1019173.
; 2000DE-1032529.
; 2000DE-1043826.
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                                                                                                                                                                                                                                                                                                                                                                                                 ID No 304; 26pp; English.
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Sequence 6107 BP; 1604 A; 136 C;

1251 G;

3116 T;

0 other;

Similarity

5.18; 47.88;

Score 56.6; Pred. No. 0.

DB 24; .044;

Length 6107;

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ABK31431/c
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signal transduction associated genes. The DNA sequences are chemical modified using a solution of bisulphite, hydrogen sulphite or disulphite. Also disclosed are oligonuclated and/or pNA oligomers for detecting the cytosine methylation state (CpG islands) of these genes, and a method for the diagnosis and/or therapy of genetic and
                                                                                                         Claim
                                                                                                                                    Oligonucleotide for diagnosis and therapy of diseases associated with signal transduction e.g. cancer, comprises chemically modified genomic sequences of genes associated with signal transduction -
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 4651
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                                                                            The present invention relates to chemically modified DNA sequences
                                                                                                                                                                                                                                                                                    30-JUN-2000;
01-SEP-2000;
                                                                                                                                                                                                                                                                                                                               29-JUN-2001; 2001WO-EP07472.
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                                                                                                                                                                                                                                                                                                                                                                                                                      Synthetic
                                                                                                                                                                                                                                                                                                                                                                                                                                                               antitumour; cytostatic; mutant;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Human;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Signal transduction associated
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Note: The sequence data for this patent did not form part of the specification, but was obtained in electronic format directly from the specification.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                epigenetic parameters of genes associated with signal transduction. The genomic DNA can be obtained from cells or cellular components which contain DNA, e.g. cell lines, biopsies, blood, sputum, stool, urine, cerebral-spinal fluid, tissue embedded in paraffin such as tissue from eyes, intestine, kidney, brain, heart, prostate, lung, breast or liver, histologic object slides, and all their possible combinations. The sequences of the invention are useful for the diagnosis and therapy of diseases associated with signal transduction e.g. solid tumours and cancer. ABK31158-ABK31545 represent chemically pretreated genomic DNA sequences of different genes associated with signal transduction, or
                                           14-MAY-1998;
                                                                        13-MAY-1999;
                                                                                                 18-NOV-1999
                                                                                                                                                            Homo
                                                                                                                                                                                       oestrogen
                                                                                                                                                                                                       breast cancer;
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                                                                                                                                                                                                   oestrogen receptor-positive breast cancer; therapy;
                                                                        99WO-US10602
                                                                                                                                                                                                                   cancerous state;
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                                                                                                                                                                                       lung cancer; ss.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     The polynucleotides sequences can be used in a method for detecting differentially expressed genes correlated with a cancerous state of a mammalian cell. The polynucleotides can also be used as probes for detecting and mapping related genes. They can be used in diagnosis and prognosis of diseases and disorders (e.g. identification of pre-metastatic or metastatic cancerous states, stages of cancer, or responsiveness of cancer to therapy). This is particularly for breast cancer, oestrogen receptor-positive breast cancer, oestrogen receptor-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            AAA00010 to AAA02716 represent polynucleotides isolated from cDNA libraries constructed from human colon cancer cell lines. The present invention also describes a method of detecting differentially expressed genes correlated with a cancerous state of a mammalian cell, comprising detecting at least one differentially expressed gene product in a test sample derived from a cell suspected of being cancerous, where detection of the differentially expressed gene product is correlated with a cancerous state of the cell from which the test sample was derived.
                                 ABL32803;
                                                               ABL32803
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42.6%;
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                                                                                                                                                                                                                                                                                            5823
                                                                                                                                                                                                                                                                                                                                                                                                                                 The present invention provides a number of human immune system associated genes which are modified by the methylation of cytosines. The sequences can be used in the diagnosis and treatment of immune system disorders, including eye diseases such as retinopathy, neovascular glaucoma and macular degeneration, arteriosclerosis, anaemia, cancer, acute myeloid leukaemia, Alzheimer's disease, AIDS, epilepsy, neurofibromatosis, rheumatoid arthritis, psoriasis and inflammatory/ulcerative bowel diseases. The present sequence is a gene of the invention.
                                                                                                                                                                                                                                                                                                                                                                                                       Sequence 6113 BP; 1694 A; 157 C; 1445 G; 2817 T; 0 other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Nucleic acid comprising fragment of chemically modified for diagnosis and treatment of diseases associated with cytosine methylation
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Claim 1; SEQ ID NO 776; 32pp + Sequence Listing;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Olek A,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               WPI; 2002-130909/17.
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01-SEP-2000;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Human; immune system disease; cytosine methylation; antiasthmatic; antiarteriosclerotic; antianaemic; cytostatic; nootropic; neuroprotective; anti-HIV; anticonvulsant; ophthalmological; antirheumatic; antiarthritic; antidiabetic; antipsoriatic; antilnflammatory; cancer; eye disease; arteriosclerosis; anaemia; acute myeloid leukaemia; Alzheimer's disease; AIDS; epilepsy;
                                                                                                                                                                                                        126
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        (EPIG-) EPIGENOMICS AG.
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                                                                                                                                   TACGCGCTCAAAGTATGTTATCTAGTAGGTGTAATTAATAATGCATGGTGCGATT 240
                                                                                                                                                                                                                                                     ACAGAAACTTCCAAATTTTTTTTTTTTTTTTGGAACAAGAAATAACAGATAGAAAACTATTT 125
                                                                                                                                                                                                                                                                                  TCTCTTTAAAAAAATTCATAAAATAAATAAACATAATATTTTATTTTATACGTATCTA
                                                                                                                                                                                           TGTTGTGGAATGGAAGTAATATATACATTAAGCAAATTTAAAAAATTATATAAGCCTA 185
                                                                                                                                                                                                                          immune system associated gene SEQ ID NO:
                                                                                                                                                                                                                                                                                                                                                                   Similarity
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                                                                                                                                                                                                                                                                                                                                                  Conservative
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2000DE-1043826
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51.9%;
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                                                                                                                                                                                                                                                                                                                                                Score 54.2; DB 24;
Pred. No. 0.13;
0; Mismatches 113;
                                      BP.
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                                                                                                                                                                                                                                                                                                                                                    Sequence
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for diagnosis and treatment
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        antiinflammatory; cancer; eye disease; arteriosclerosis; anaemia;
acute myeloid leukaemia; Alzheimer's disease; AIDS; epilepsy;
neurofibromatosis; rheumatoid arthritis; psoriasis; bowel disease
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             antiarteriosclerotic; antianaemic; cytostatic; nootropic;
neuroprotective; anti-HIV; anticonvulsant; ophthalmological;
antirheumatic; antiarthritic; antidiabetic; antipsoriatic;
                                                                                                                                                                                                                                                                                                                                                                        rheumatoid arthritis, psoriasis and inflammatory/ulcerativ diseases. The present sequence is a gene of the invention.
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01-SEP-2000;
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AATGTGTTTTCTGACTA
                           AAATTATTAATATTTAGTCAATAACAATGCATAGAAAGTTCCAAAAAAATTTTGTTAAC 67
                                                                                                                                  GTTGTGGAATGGAAGTAGTAATATACATTAAGCAAATTTTAAAAAATTATATAAGCCTAT 186
                                                                                                                                                                                                                AGAAACTTCCAAATTTTTTTTTTTTTTTTTGGAACAAGA-AATAACAGATAGAAAACTATTTT 126
                                                                                                      ACGCGCTCAAAGTATGTTATCTAGTAGGTGTAATTAATAATGCATGGTGCGATTCAGAAT 246
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                                                                                                                                                                                                                                                                                                             Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    EPIGENOMICS AG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                SEQ ID NO 2170; 32pp + Sequence Listing; German.
                                                                                                                                                                                                                                                                                                                                                    37973 BP;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           methylation
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                                                                                                                                                                                                                                                                                               4.9%;
llarity 50.2%;
Conservative
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2000DE-1043826.
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                                                                                                                                                                                                                                                                                                                                                     10756 A;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    disease; cytosine methylation;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       fragment of chemically modified ment of diseases associated with
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                                                                                                                                                                                                                                                                                                                                                     620 C;
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); Mismatches
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Best Local :
                                                                                                                                                                                                                      74888
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    bases of chemically pretreated DNA of angiogenesis-associated genes (II) having sequences (ABQ66971-ABQ67178) or their complements. (I), also related oligomers, are used to evaluate the methylation status and/or single-nucleotide polymorphisms, in angiogenesis-related genes, for diagnosis and treatment of eye diseases, proliferative retinopathy, neovascular glaucoma, solid tumours, inflammation, rheumatoid arthritis, diabetic retinopathy, macular degeneration caused by neovascularisation,
                                                                                                                                                                                                                                                                                                                                                                                                                                          Sequence 83391 BP; 24547 A;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Note: The sequence data for this patent did not form specification, but was obtained in electronic format
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          New nucleic acid fragments from chemically treated angiogenesis-associated genes, useful for determin status, e.g. in diagnosis or treatment of cancer
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           8117
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Crohn's disease.
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                                                                                                                                                          GAAACTTCCAAATTTTTTTTTTTTTTATGGAACAAGAATAACAGATAGAAAACTATTTTGT 128
                                                                                                                                                                                                                TGTGGAATGGAAGTAGTAATATACATTAAGCAAATTTTAAAAAATTATATAAGCCTATAC 188
                                                                                                      AATTATTAATATTTAGTCAATAACAATGCATAGAAAGTTCCAAAAAAATTTTGTTAACA 68
AGTAG - AGAAATGATTACGTAAATAATAATAGTATTTTATATAATAGAATAGTATGAAG
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                                                                                                                                                                                                                                                                                                                                Conservative
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49.5%;
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                               6867
                                                                                                                                                                                                                                         The present invention provides a number of human immune system associated genes which are modified by the methylation of cytosines. The sequences can be used in the diagnosis and treatment of immune system disorders, including eye diseases such as retinopathy, neovascular glaucoma and leukaemia, Alzheimer's disease, AIDS, epilepsy, neurofibromatosis, the present sequence is a gene of the invention.
                                                                                                                                                                                                                      Sequence 17131 BP;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Claim 1; SEQ ID NO 1026;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       for diagnosis and treatment of diseases associated with
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01-SEP-2000;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    antirheumatic; antiarthritic; antidiabetic; antipsoriatic;
antiinflammatory; cancer; eye disease; arteriosclerosis; a
acute_myeloid leukaemia; Alineimer's disease; AIDS; epilep
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Human; immune system disease; cytosine methylation; antiasthmatic; antiarteriosclerotic; antianaemic; cytostatic; nootropic; neuroprotective; anti-HIV; anticonvulsant; ophthalmological;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 75187
                                               28 ATAACAATGCATAGAAAGTTCCAAAAAAATTTTGTTAACAGAAACTTCCAAATTTTTTT 87
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             W0200200928-A2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Homo sapiens.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 neurofibromatosis;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Human immune system associated gene SEQ ID
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     26-MAR-2002
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ABL33053;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ABL33053 standard;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 309
2002-130909/17.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   TTATTAATATTAATGGAAAAATATAGGTTATAAAATTATATAGAATTTAATTTAATTTAT 75186
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              TGTGTTTTCTGACTATTGAGGGGCAAAAAAAAG
                                                                                                                                                 Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            methylation
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Piepenbrock C,
                                                                                                                    Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              2000DE-1032529
2000DE-1043826
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                (first entry)
                                                                                                                                                                                                              5134 A;
                                                                                                                                       4.9%;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               DNA; 17131
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Berlin
                                                                                                                                                                                                      253 C; 3328 G; 8413 T;
                                                                                                            Score 53.4; DI
Pred. No. 0.22,
0; Mismatches
                                                                                                                 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ВP
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                                                                                                                                       DB 24;
1.22;
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                                                                                                    Indels
                                                                                                                                                       Length 17131;
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nabnormal
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RESULT 10
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                                                                                                                                                                                                                                                      06-APR-2000;
07-APR-2000;
30-JUN-2000;
01-SEP-2000;
                                                                                                                         New nucleic acids or oligomers, useful for diagnosing or treating diseases associated with DNA transcription, e.g. immunological disorders, Werner syndrome, psoriasis, myocardial infarction, solid
                                                                                                                                                                                     WPI;
                                                                                                                                                                                                            OLek
                                                                                                                                                                                                                                                                                                                                                                                                        PNA; cytosine methylation state; SNP; retroviral infection; gene; ds; viral infection; serie; ds; viral infection; Sezary syndrome; adenosine deaminase deficiency; cancer; inmunological disorder; werner syndrome; developmental disorder; tuberculosis; psoriasis; Rieger's syndrome; neurological disorder; erythropoiesis; neurodegenerative disorder; meurological disorder; erythropoiesis; myelodysplastic syndrome; myocardial infarction; hypertension; arthritis; angiogenesis; congenital heart disease; HDR syndrome; gene therapy;
                                                                                                                                                                                                                                                                                                            06-APR-2001; 2001WO-EP03973
                                                                                                                                                                                                                                                                                                                                       06-DEC-2001.
                                                                                                                                                                                                                                 (EPIG-)
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                                                                                                                                                                                                                                                                                                                                                                                    Unidentified.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            DNA transcription associated gene;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                DNA transcription associated genomic DNA #66.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        6627
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               TAGTAGGTGTAATTAATAATGCATGGTGCGATTCAGAATTGGGACAACAATGAAAACGGA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        TTTTTATGGAACAAGAATAACAGATAGAAAACTATTTTGTTGTGGAATGGAAGTAGTAA 147
                                                                                                                                                                                                                               EPIGENOMICS
                                                                                                                                                                                                       Piepenbrock C,
                                                                                                                                                                                                                                                    ; 2000DE-1019058.
; 2000DE-1019173.
; 2000DE-1032529.
; 2000DE-1043826.
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                                                                                                                                                                                                                               ĀG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            DNA;
                                                                                                                                                                                                      Berlin
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                                                                                                                                                                                                      ζ,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 e; peptide nucleic acid; PNA-oligomer; SNP; retroviral infaction.
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The invention relates to a nucleic acid, which comprises a segment of the chemically pretreated DNA of genes associated with DNA transcription from one of 346 sequences, and an oligomer, in particular an oligonucleotide to the chemically pretreated DNA of genes associated with DNA transcription. The set of oligomer that hybridises to or is identical transcription. The set of oligomer probes are useful for detecting the cyrosine methylation state and/or single nucleotide polymorphisms (SNPs) in a chemically pretreated genomic DNA. The nucleic acids are useful for

Claim 1;

SEQ

IJ

No 131; 32pp;

English.

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Note: The sequence data for this pattent did not form part of the printed specification but was obtained in electronic format directly from the European Patent Office.
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Best Local
                                                                                                                                                                                                                                                                                                                                                                             lipid-associated condition; arteriosclerosis; cardiovascular disease; ss; osteoporosis; atherosclerosis; diabetic atherosclerosis; plaque build-up; neurovascular condition; wound healing; gene therapy; PCR primer; probe; bone development disorder; antiarteriosclerotic; cardiovascular;
                             26-MAY-2000;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Human; mouse; Zmax1; HBM; high bone mass gene; lipid regulation; stroke;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ABK22782 standard; cDNA; 54108
                                                                                            25-MAY-2001;
                                                                                                                                                                                                                         WO200192891-A2
                                                                                                                                                                                                                                                                                                                                                      osteopathic;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Human high bone mass (HBM) polynucleotide clone #5.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               311
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     CTCATTGGTTAGTTTAAGCTTAATAAGAAGATTTTATTAAATTTTAATGACGATGATAAC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           CAAAAATTAGAAAATATAAATATGAAAAATAGAGGAAAAGAGGTTTTAATTTTATATATA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Similarity 47.8
54; Conservative
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                                                                                            2001WO-US16946
                             2000US-0578900
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       (first entry)
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Pred. No. 0.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ВP
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                                                                                                                                                                          The invention relates to a method for identifying a molecule involved in lipid regulation comprising identifying a molecule that binds to or inhibits binding of a molecule to high bone mass (HBM) or its wild type gene, Zmax1. Compounds identified by the method are useful for treating, diagnosing, preventing or screening for normal and abnormal lipid-associated conditions, including arteriosclerosis, cardiovascular disease, stroke, and osteoporosis. The compounds may also be used in the treatment or prevention of diabetic atherosclerosis, neurovascular conditions caused by plaque build-up, poor circulation due to plaque build-up and associated poor wound healing. The methods may be used in gene therapy, pharmaceutical development, and dispostic assays for bone development disorders. Molecules identified by comparison of Zmax1 and HBM systems can be used as surrogate markers in pharmaceutical development, in diagnosis of fuman or animal bone disease, and in the treatment of bone diseases. Sequences ABK22776-ABK23411 represent cDNA molecules encoding human Zmax1 and HBM, and PCR primers, probes, linkers and adapters of the invention.
                                                                   Query Match
Best Local
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 diagnosing, treating or preventing e.g., arteriosclerosis, comprises identifying a molecule that binds to high bone mass gene or its corresponding wild type gene \,
                                                                                                                                       Sequence 54108 BP; 11394 A; 14471 C; 15121 G; 13120 T; 2 other
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Example 2;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Identifying molecules involved in lipid regulation, useful for
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      (GENO-) GENOME THERAPEUTICS CORP. (UYCR-) UNIV CREIGHTON SCHOOL MEDICINE.
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                                                                      Similarity
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                                                   Conservative
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                                                                      4.8%;
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                                              Score 53; DB 24; I
Pred. No. 0.31;
0; Mismatches 155;
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RESULT 12
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         Human high bone mass (HBM) polynucleotide clone #7
                              09-APR-2002
                                                   ABK22784;
                                                                        ABK22784 standard;
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                                                                                                                                               TAAATGTGTTTTC 317
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                              (first entry)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     conditions caused by plaque build-up, poor circulation due to plaque build-up and associated poor wound healing. The methods may be used in gene therapy, pharmaceutical development, and diagnostic assays for bor development disorders. Molecules identified by comparison of Zmax1 and HBM systems can be used as surrogate markers in pharmaceutical development, in diagnosis of human or animal bone disease, and in the treatment of bone diseases. Sequences ABK22776-ABK23411 represent cDNA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Human; mouse; Zmax1; HBM; high bone mass gene; lipid regulation; stroke; lipid-associated condition; arteriosclerosis; cardiovascular disease; ss; osteoporosis; atherosclerosis; diabetic atherosclerosis; plaque build-up; neurovascular condition; wound healing; gene therapy; PCR primer; probe; bone development disorder; antiarteriosclerotic; cardiovascular;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            diagnosing, treating or preventing e.g., arteriosclerosis identifying a molecule that binds to high bone mass gene corresponding wild type gene \,
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Carulli JP,
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Identifying molecules involved in lipid regulation, useful for
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   26-MAY-2000;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Sequence 57273 BP; 12179 A; 15326 C; 15607 G; 14161 T; 0 other:
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                                                                                                                                                                                                                                                                                                                                                                                                           TTGTTGTGGAATGGAAGTAGTAATATACATTAAGCAAATTTTAAAAAATTATATAAGCCT
                                                                                                                                                                                                                                                                                                                      ACAGAAACTTCCAAATTTTTTTTTTTTTTTGGA-ACAAGAAATAACAGATAGAAAACTATT 124
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           GENOME THERAPEUTICS
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Page 350-392; 409pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     of the
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 CREIGHTON
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           human Zmaxl and HBM, and PCR primers, probes, linkers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     invention.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                4.8%;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Score 53; DB 24;
Pred. No. 0.31;
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                                    26974
                                                                                                                                                                                                                                                                                              HBM genes have osteopathic activities. The genes can be used in gene therapy, antisense therapy and in the production of vaccines. They can be used in the diagnosis and treatment of bone disorders including
                                                                                                                                                                                                                                                                          osteoporosis, Paget's disease, sclerostosis, dysplasia. ABA82038 to ABA82700 and AAG68168
                                                                                                                                                                                                                                                                                                                                    The present invention describes the human Zmax1 gene and the high bone mass (HBM) gene, which are found on chromosome 11q13.3. The Zmax1 and
                                                                                                                                                                                                                                                                                                                                                                        Claim 51; Page 308-350; 443pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                     New high bone mass (HBM)
modulating bone mass for
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               05-APR-2000;
05-APR-2000;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    antisense therapy; vaccine; bone disorder; Paget's disease, sclerostosis; osteomalacia; fibrous dysplasia; ds.
                                                                                                                                                                                                                                    Sequence 66933 BP; 14237 A; 17817 C; 18323 G; 16556 T; 0 other
                                                                                                                                                                                                                                                                                                                                                                                                  modulating
                                                                                                                                                                                                                                                                                                                                                                                                                                                                Carulli JP,
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                                                                                                                                                     ACAAATTATTAATAATATTTAGTCAATAACAATGCATAGAAAAGTTTCCTAAAAAAATTTTTGTTA
                                                           TTGTTGTGGAATGGAAGTAGTAATATACATTAAGCAAATTTTAAAAAATTATATAAGCCT 184
                                                                                    ACAGAAACTTCCAAATTTTTTTTTTTTTATGGA-ACAAGAAATAACAGATAGAAAACTATT 124
                                                                                                                                     HBM gene region b200e21-h_contig4.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           high bone mass; HBM gene; Zmax1 gene; chromosoroe tagged site; STS; osteoporosis; osteopathic;
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2000US-0544398
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Pred. No. 0.32;
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                                                                                                                                                                                                                                                              present invention.
                                                                                                                                                                                                                                                                          to AAG68193 represent
                                                                                                                                                                                                                                                                                       osteomalacia and fibrous
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                                                                                                                                                                                                             Length
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                                                                                                                                                                                                             The present invention describes the human Zmax1 gene and the high bone mass (HBM) gene, which are found on chromosome 11q13.3. The Zmax1 and HBM genes have osteopathic activities. The genes can be used in gene therapy and in the production of vaccines. They can be used in the diagnosis and treatment of bone disorders including osteoparosis, Paget's disease, solerostosis, osteomalacia and fibrous dysplasia. ABAB2038 to ABAB2700 and AAG68168 to AAG68193 represent
                                                                                                                                                                                                                                                                                                          Claim 51; Page 258-302; 443pp;
                                                                                                                                                                                                                                                                                                                                  New high bone mass (HBM) modulating bone mass for
                                                                                                                                                                                                                                                                                                                                                                                          Carulli JP, Little RD,
                                                                                                                                                                                                                                                                                                                                                                                                                                         05-APR-2000;
05-APR-2000;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Homo sapiens.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Human; high bone mass; HBM gene; Zmax1 ge
sequence tagged site; STS; osteoporosis;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ABA82623
                                                                                                                                                                              Sequence
                                                                                                                                                                                                   sequences used in the exemplification of the present invention.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         sclerostosis;
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                                                                                                                                                                            72049 BP; 15164 A; 19306 C; 20142 G; 17434 T; 3 other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       standard; DNA; 72049 BP.
                                                                                                                                 Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                         2000US-0543771.
2000US-0544398.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      osteomalacia; fibrous dysplasia; ds.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   vaccine;
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                                                                                                                                         Score 53; I
Pred. No. 0.
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                                                                                                                                                                                                                                                                                                            English.
                                                                                                                               Mismatches
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porosis; osteopathic; gene 1
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                                     CC The invention relates to a nucleic acid comprising a sequence of at least CC 18 bases of a segment of chemically pretreated DNA of genes associated CC with cell signalling. The activity of the modified sequences of the CC invention may be described as cytostatic. The object of the invention is CC to provide the chemically modified DNA of genes associated with cell city signalling, as well as oligonucleotides and/or PNA-oligomers for CC detecting cytosine methylations, as well as a method which is CC particularly suitable for the diagnosis and/or therapy of genetic and CC epigenetic parameters of genes associated with cell signalling. The CC chemically modified DNA provided by the invention is useful for diagnosis and therapy of diseases such as solid tumours and cancer. The sequences CC genemic DNA's of genes associated with cell signalling.

CC Note: The sequence data for this patent is not represented in the printed CC specification, but is based on sequence information supplied by the
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                                                                                                                                                                                                                                                                                              Claim 1; SEQ ID NO 349; 24pp+sequence listing; English.
                                                                                                                                                                                                                                                                                                                        Nucleic acid, useful for diagnosis and therapy of diseases associated with cell signalling e.g. cancer, comprises chemically modified genomic sequences of genes associated with cell signalling \,
                                                                                                                                                                                                                                                                                                                                                                                           WPI;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Cell signalling; cytosine methylation; cell signalling disease; cancer; tumour; cytostatic; ds.
                             European Patent
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01-SEP-2000;
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Best Local Matches 1 Query Match

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Score 52.6; I Pred. No. 0.31 0; Mismatches

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Search completed: March 29, 2003, 18:32:56 Job time: 644.917 secs

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1: /cgn2_6/ptodata/1,
2: //gn2_6/ptodata/1,
3: /cgn2_6/ptodata/1,
4: /cgn2_6/ptodata/1,
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/cgn2_6/ptodata/1/ina/6L_COMB.seq:*
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5 US-08-607-860B-32
5 US-08-607-956-102
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Sequence 3, Appli Sequence 13, Appli Sequence 137, Appli Sequence 136, Appli Sequence 1651, Appli Sequence 1651, Appli Sequence 14, Appli Sequence 14, Appli Sequence 14, Appli Sequence 2, Appli Sequence 32, Appli Sequence 32, Appli Sequence 32, Appli Sequence 33, Appli Sequence 32, Appli Sequence 34, Appli Sequence 37, Appli Sequence 38, Appli Sequence 39, Appli Sequence 8, Appli Sequence 8, Appli Sequence 10, Appli Sequence 15, Appli Sequence 17, Appli Sequence 17, Appli Sequence 17, Appli Sequence 102, Appl
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Sequence 1, Appli	Sequence 63 Appl		Segmence 2 Appli	Sequence 2 Appli		Segmence 1 Appli		- !	- ;	Sequence 595 Ann	ָל ע	100		100	103		Seguence 100 App

## ALIGNMENTS

ORIGINAL SOURCE: ORGANISM: Brassica napu IMMEDIATE SOURCE: LIBRARY: genomic Lambda CLONE: BnACCaseg10 FEATURE: NAME/KEY: Startcodon LOCATION: 26112613 FEATURE: NAME/KEY: CDS	TTE: 01-MAR-CATION DATA: ON NUMBER: ON NUMBER: ON NUMBER: TE: 04-SEP- OR SEQ ID NO ARACTERISTIC 3350 Base pa cleic acid ESS: Double ESS: DNA (9e L: NO	140 Avenue York York USA 6 6 Chable FORM. E: Diskett E: Diskett E: Diskett IBM Compat SYSTEM: DO Patentin PA N NUMBER:	RESULT 1  US-08-617-860B-3/c  Sequence 3, Application US/08617860  Patent NO. 613506  GENERAL INFORMATION:  APPLICANT: Typfer, R., Bautor,  APPLICANT: Hyricke-Grandplerre,  APPLICANT: M ller, A., Schulte,  APPLICANT: Schell, J.  TITLE OF INVENTION: Promoters  NUMBER OF SEQUENCES: 35  CORRESPONDENCE ADDRESS:  CORRESPONDENCE ADDRESS:
napus ambda FIX II on 3	TA: 1996 TA: PCT/EP94/02950 EP-1994 EP-1993 EP-1993 INC: 3: INC: 3:	e of the Americas  M: tte, 3.50 inch, 1.4 Mb storage atible DOS Release #1.0, Version #1.25 (EPO) ATA: US/08/617.860B	B J., Bothmann, C., Klein, B. W., Voetz, M.

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                                                                                                                                                                                                                                                                                                                                                                          SEQ ID NO 3
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Best Local
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APPLICANT: Murphy, Judith B.

APPLICANT: The Regents of the University of California

TITLE OF INVENTION: A NO. 6465716 Factor Binding Protein From Legume Roots

FILE REFERENCE: 023070-079810457
                                                                                                                                                                                                                                                                                                                                                                                                                                             CURRENT APPLICATION NUMBER: US/09/129,112
CURRENT FILING DATE: 1998-08-04
PRIOR APPLICATION NUMBER: US 08/907,226
                                                                                                                                                                                                                                                                                                                                                                                                             NUMBER OF SEQ ID NOS: 19
                                                                                                                                                                                                                                                                                                                                                                                           SOFTWARE:
                                                                                                                                                                                                                                                                                                                                                                                                                                PRIOR FILING DATE:
                                                                                                                                                                                                                                         NAME/KEY: exon LOCATION: (633
                                                                                                                                                                                                                                                                                                              ORGANISM: Dolichos biflorus
                                                                         NAME/KEY:
                                                                                                                                                                                                                                                                           OTHER INFORMATION: genomic sequence of NBP46 (DB46)
                                                                                                                                                                                                                                                                                                                                     TYPE: DNA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               AATTGTCAATAACAGAAATAAACTAACACC 1925
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          AAGAGTTATGATATAAAAAAAATCAAGACATAAAATTTATAAATATTTAAATATTTAAT 2015
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     AAATGTGTTTTCTGACTATTGAGGGGCAAAAAAAAAAGACAATGCCAAAAGTCTACGGGTTT 365
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             TACGCGCTCAAAGTATGTTATCTAGTAGGTGTAATTAATAATGCATGGTGCGATTCAGAA 245
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ACTAAAATTTAATAATTTAAAATGTTTTTAAAACATAAAATAATAGTTTGGGTA-TGTAT 2195
                                                                                                                                                                                                                                                                                                                                                                                           PatentIn Ver. 2.1
                                                                                                             exon
                                                                                                                                                                                                      (945)..(1022)
                                                    (1617)..(1697)
                                                                                        (1560)..(1616)
                                                                                                                                                                 (1023)..(1151)
               (1698)..(1790)
                                                                                                                                                                                                                                         (633)..(944)
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                                                                                                                                                                                                                                                                                                                                                                                                                                1997-08-06
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48.7%;
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Best Local
                        INFORMATION FOR SEQ ID NO: 1:
SEQUENCE CHARACTERISTICS:
SEQUENCE: 19124 base pairs
TYPE: nucleic acid
                                                                                                               REFERENCE/DOCKET NUMBER: NI
TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                        CURRENT APPLICATION DATA:
APPLICATION NUMBER: US.
FILING DATE: 10-SEP-19
                                                                                                                                                                                                                                                                                             COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
                                                                                                                                                                                                                                                                                                                                                                                                                  CORRESPONDENCE ADDRESS
                                                                                                                                                                                                                                                                                                                                                                                                                                               TITLE OF INVENTION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                     APPLICANT: Wellems, Thomas E.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    APPLICANT:
APPLICANT:
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                                                                                                                                                                               CLASSIFICATION: 435
                                                                                                                                             REGISTRATION NUMBER:
                                                                                                                                                                                                                                                                 COMPUTER: IBM PC compatible OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                         CITY: Newport Beach
STATE: California
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             STRANDEDNESS:
                                                                                                  TELEPHONE:
                                                                                                                                                                NAME:
                                                                                                                                                                                                                                                  SOFTWARE: PatentIn Release #1.0, Version #1.25
                                                                                                                                                                                                                                                                                                                                           COUNTRY:
                                                                                                                                                                                                                                                                                                                                                                                                  ADDRESSEE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             TCACAACAAGTTTGAAATTTAAAAACTATATTATAAATATTACCAAATACATTTTAT
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                TGTTTTCTGACTATTGAGGGGCAAAA 336
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          TCAAAGTATGTTATCTAGTAGGTGTAATTAATA--ATGCATGCGATTCAGAATTGGG 250
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ATGGAAGTAGTAATATACATTAA--GCAAATTTTAAAAAATTATATAAGCCTATACGCGC 192
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     TCCAAATTTTTTTTTTTTTATGGAACAAGAATAACAGATAGAAAACTATTTTGTTGTGGA 134
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          TCTTTTTTTTTTTTTTTTGAAAATGTTTTGAAATATTGTCAAATATTAATAGTGA 2818
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                                                                                                                                                             Israelsen, Ned
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                                                                                                                                                                                                                                                                                                                                                                                      620 Newport Center Drive
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Miller, Louis H
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O Newbort Center Drive 16th Floor
linear
                                                                                                    (619)
          single
                                                                                   9) 235-8550
235-0176
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AND PLASMODIUM FALCIPARUM ERYTHROCYTE BINDING PROTEINS
45
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       David S.
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                                                                                                                                                                                                                    US/08/487,826B
                                                                                                                                             29,655
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Pred. No. 0.023;
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RESULT 4
US-08-998-416-1137/c
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Patent No.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Query Match
Best Local Similarity
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                       INFORMATION FOR SEQ ID NO:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        15855 АЛААЛАЛААТАЛТАЛАТАЛААЛАЛТТТАЛТТАЛТЛАЛАЛАЛАЛТТАЛАЛАЛАЛТТАЛТС 15914
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                                                                          ATTORNEY/AGENT INFORMATION:
NAME: Meigs, J. Timothy
REGISTRATION NUMBER: 38,241
REFERENCE/DOCKET NUMBER: PF
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                          SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                              MEDIUM TYPE: Floppy
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  MOLECULE TYPE:
HYPOTHETICAL:
ANTI-SENSE: NO
                                                                                                                                                        PRIOR APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                     CORRESPONDENCE ADDRESS
                                                                                                                                                                                                                                                                                                                                                                                                 TITLE OF INVENTION:
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                                                                                                                                                                      FILING DATE: 24
CLASSIFICATION:
                                                                                                                                                                                APPLICATION NUMBER: US/08/998,416
FILING DATE: 24-DEC-1997
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 APPLICATION NUMBER: CH 0
FILING DATE: 31-DEC-1996
                                                                                                                                                                                                                                     MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                       COUNTRY:
                                                                                                                                                                                                                                                                                                                                                            ADDRESSEE:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     GCGCTCAAAGTATGTTATCTAGTAGGTGTAATTAATAATGCATGGTGCGATTCAGAATTG 248
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        INFORMATION:
                                                                                                                                                                                                                                                                                                                T: 3054 Cornwallis Road
Research Triangle Park
: No. 6239264th Carolina
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                                       919-541-8689
                                                                                                                                                                                                                                                                                                                                                                          Wendland, Jurgen
Knechtle, Philipp
Rebischung, Corinne
VENTION: GENOMIC DNA SEQUENCES OF ASHBYA GOSSYPII
VENTION: AND USES THEREOF
                                                                                                                                                                                                                                                                                                        USA
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Steiner, Sabine
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Philippsen, Peter
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Mohr, Christine
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                                                                                                                                           CH 0016/97
                                                                          PF/5-30306/A/CGC1976
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Pred. No. 0.12;
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Query Match
Best Local Similarity
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                                                                                 TYPE: N
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US-08-451-405A-2
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GENERAL INFORMATION:
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                                                                                                                                                                                                                                                                               FILING DATE: 15-JAN-1
                                                                                                                                                                                                                                                  SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                           PRIOR APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             COMPUTER READABLE FORM: MEDIUM TYPE: 3.5" FL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               CORRESPONDENCE ADDRESS:
ADDRESSEE: THE WEBB
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              TITLE OF INVENTION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      APPLICANT: FASEL, NI
APPLICANT: REYMOND,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             MOLECULE TYPE:
ORIGINAL SOURCE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                NUMBER OF SEQUENCES:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 DISK Midwest Micro 486-50 OPERATING SYSTEM: DOS SOFTWARE: WORDDOOR OF THE PROPERTY OF THE PROP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       396 ATAAAAATAATAATTT 381
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            226 ATGCATGGTGCGATTCAGAATTGGGACAACAATGAAAACGGAATTAAAATATTAACTTTA 285
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                STRANDEDNESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     APPLICATION NUMBER: US/O
FILING DATE: 26-MAY-1995
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        106 TAACAGATAGAAAACTATTTTGTTGTGGAATGGAAGTAGTAATATACATTAAGCAAATTT 165
                                                                                                                                      TOPOLOGY:
                                                                                                                                                                                                                                                                                                      APPLICATION NUMBER: 07/9 FILING DATE: 15-JAN-1993
                                                                                                                                                                                                                                                                                                                                                                                                               CLASSIFICATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    CITY: PITTSBURGH
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Local Similarity
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700 KOPPERS BUILDING, 436 SEVENTH
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Score
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No.
DB 1;
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                          Length 731;
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DB 2;

Length 665;

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RESULT 6
US-08-883-795A-36
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US-08-883-795A-36
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                                                                                                                                   INFORMATION FOR SEQ ID NO:
                                            MOLECULE TYPE:
ORIGINAL SOURCE:
                                                                                                                                                                REGISTRATION NUMBER: 40,261
REFERENCE/DOCKET NUMBER: 78
TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                 APPLICATION NUMBER: US/01
FILING DATE: 27-JUN-1997
CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                   SOFTWARE: Patentin Rel
CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                          COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                             APPLICANT: Delcuve, Genev
                    IMMEDIATE SOURCE:
                                                                                                                      SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                  CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                          TITLE OF INVENTION:
                                                                                                                                                                                                                                                                                                                                                                                                                                NUMBER OF SEQUENCES:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    195
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                                   ORGANISM:
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                                                                     TOPOLOGY:
                                                                                STRANDEDNESS:
                                                                                                                                                                                                         NAME: Gravelle, Micheline
                                                                                                                                                                                                                                                                                                                                                      COUNTRY:
                                                                                                                                                                                                                                                                                                                                                                               CITY: Toronto
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                                                                                                        LENGTH:
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                                                                                                                                                                                                                                                                                Release #1.0, Version #1.25
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Best Local Similarity
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US-08-947-823-1
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Patent No. 6114605
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                                                                                                                                                                                                                                                                        OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
                                                                                                                                                                                                  PRIOR APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                             COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             NUMBER OF SEQUENCES: 5
                                                       FILING DATE: 10-OCT-1996
ATTORNEY/AGENT INFORMATION:
NAME: Bastian, Kevin L.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        TITLE OF INVENTION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   APPLICANT:
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                                                                                                                                     PRIOR APPLICATION DATA:
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                                 NAME: Bastian, Kevin L. REGISTRATION NUMBER: 34,774
                                                                                                                                                          APPLICATION NUMBER: PCT/
FILING DATE: 09-OCT-1997
                                                                                                                                                                                                                         CLASSIFICATION:
                                                                                                                                                                                                                                          APPLICATION NUMBER: US/08/947,823 FILING DATE: 09-OCT-1997
                   REFERENCE/DOCKET NUMBER:
                                                                                                                  APPLICATION NUMBER:
                                                                                                                                                                                                                                                                                                                                              COMPUTER:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                   STATE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                      CITY: San Francisco
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       STREET:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ADDRESSEE:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ATGTTTATAATT - - - - - ACATATTTTATAATTAAAATGTTTATAATTACATATTTTATAA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ACTATTAGCCAGAGACAATTGATTATAGATATATCCATTAATCCATGATATTTATGATAT 765
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                                                                                                                                                                                                                                                                                                                                                                                                                                                 California
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Two Embarcadero Center, Eighth Floor
                                                                                                                                                                                                                                                                                                                                                                                                                              USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Milligan, Stephen
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Williamson, Valeri
Kaloshian, Isgouhi
Yaghoobi, Jafar
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Bodeau, John
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Conservative
                                                                                                                                                                                                                                                                                                                         IBM PC compatible
SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Townsend and Townsend and Crew LLF
INFORMATION
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Procedures and Materials for Conferring Pest Resistance in Plants
                                                                                                                    US 60/028,191
                                                                                                                                                                             PCT/US97/18802
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                   023070-070210US
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TELEPHONE:

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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    US-09-641-638-651/c
                                                                                                                              SOFTWARE: Pate
SEQ ID NO 651
LENGTH: 20674
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Sequence 651, Application US/09641638 Patent No. 6432648
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Matches 170;
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Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                           APPLICANT: Cohen, Annick
TITLE OF INVENTION: BIALLELIC MARKERS DERIVED FROM GENOMIC REGIONS CARRYING
TITLE OF INVENTION: GENES INVOLVED IN ARACHIDONIC ACID METABOLISM
FILE REFERENCE: GENSET.051CP1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  TELEFAX: (415) 576-0300 INFORMATION FOR SEQ ID NO:
                                                                                                                                                                                                         PRIOR FILING DATE: 2000-02-11
PRIOR APPLICATION NUMBER: US 60/133,200
PRIOR FILING DATE: 1999-05-07
PRIOR APPLICATION NUMBER: US 09/275,267
PRIOR TILING DATE: 1999-03-23
PRIOR APPLICATION NUMBER: US 60/119,917
PRIOR APPLICATION NUMBER: US 60/119,917
PRIOR FILING DATE: 1999-02-12
                                                                                                                                                                                                                                                                                                                                             CURRENT APPLICATION NUMBER: US/09/641,638
CURRENT FILING DATE: 2000-08-16
PRIOR APPLICATION NUMBER: US 09/502,330
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      APPLICANT:
                                                                                                                                                                                          NUMBER OF SEQ ID NOS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    APPLICANT:
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NAME/KEY: misc_feature
LOCATION: 1123..3123
OTHER INFORMATION: 5'regulatory region
NAME/KEY: exon
                                                                          FEATURE:
                                                                                            ORGANISM: Homo sapiens
                                                                                                                TYPE: DNA
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LENGTH: 51952 base pairs
TYPE: nucleic acid
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        GCCTATACG-----CGCTCAAAGTATGTTATCTAGTAGGTGTAATTAATAATGCATGGTG 235
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              TATTTTGTTGTGGAATGGAAGTAGTAATATACATTAAGCAAATTTTAAAAAATTATATAA 180
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          TAAAGAATTCTTATGTAAACATATGTTAATATTTGTTACAGAATATGACCACTAAATTCG 32652
                                                                                                                                                                      Patent.pm
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nilarity 47.68;
Conservative
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BER: US 09/502,330
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NAME/KEY: allele
LOCATION: 2323
OTHER INFORMATION:
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OTHER INFORMATION:
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LOCATION: 1559
OTHER INFORMATION: 10-509-284
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LOCATION: 17555..20674
OTHER_INFORMATION: 3'regulatory region
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OTHER INFORMATION: exon
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OTHER INFORMATION: exon
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NAME/KEY: allele LOCATION: 2832
                            OTHER INFORMATION: 10-512-318
                                        NAME/KEY: allele
LOCATION: 2623
                                                                       OTHER INFORMATION:
                                                                                                    NAME/KEY: allele
                                                                                                                                                                                                      LOCATION: 1827
OTHER INFORMATION: 10-510-173
                                                                                                                                                                                                                           NAME/KEY: allele
LOCATION: 1827
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OTHER INFORMATION:
                                                                                                                                                                                                                                                                                 NAME/KEY: allele
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                                                                                                                                                                                                                                                                                                                                                           NAME/KEY: allele
LOCATION: 1182
                                                                                                                                                                                                                                                                                                                                                                                       OTHER INFORMATION: 10-508-191 : polymorphic base C
                                                                                                                                                                                                                                                                                                                                                                                                       NAME/KEY: allele
LOCATION: 1128
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                OTHER INFORMATION: exon
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LOCATION: 13308..13429
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LOCATION: 12854..13023
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                                                                                    OCATION: 2341
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                                                                                                                   insertion of
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NAME/KEY: allele LOCATION: 6429
OTHER INFORMATION: 1
NAME/KEY: allele LOCATION: 6467
OTHER INFORMATION: 1
NAME/KEY: allele LOCATION: 6484
OTHER INFORMATION: 1
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OTHER INFORMATION:
            NAME/KEY: allele
LOCATION: 8777
                                           NAME/KEY: allele
LOCATION: 8703
                                                                    LOCATION: 8658
OTHER INFORMATION:
                                                                                                   NAME/KEY: allele
LOCATION: 8608
OTHER INFORMATION:
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LOCATION: 6375
OTHER INFORMATION:
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OTHER INFORMATION: 10-343-339
NAME/KEY: Bllele
LOCATION: 5903
OTHER INFORMATION: 10-346-23
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LOCATION: 3802
OTHER INFORMATION:
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LOCATION: 2934
OTHER INFORMATION:
                                   OTHER INFORMATION:
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LOCATION: 6611
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LOCATION: 6338
OTHER INFORMATION:
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OTHER INFORMATION:
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LOCATION: 4088
OTHER INFORMATION:
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LOCATION: 2947
OTHER INFORMATION:
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LOCATION: 6534
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LOCATION: 6183
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LOCATION: 6141
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LOCATION: 6019
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OTHER INFORMATION:
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INFORMATION:
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                                   10-349-142
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Best Local :
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                              APPLICANT: Slade, Mart APPLICANT: Chang, Andy APPLICANT: Williams, K TITLE OF INVENTION: SI TITLE OF INVENTION: SI NUMBER OF SEQUENCES: 1
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LOCATION:
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STREET:
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            ADDRESSEE:
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Chang, Andy C M
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Improved Plasmid Vectors for Cellular
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COMPUTER READABLE FORM: MEDIUM TYPE: Floppy

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ZIP: COUNTRY:

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USA

CITY:

Philadelphia

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US-07-867-106-4
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Best Local Similarity
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         SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/487,826B
                                                       COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
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                                                                                                                                                                                                                                                                                                                                                                                  tent No.
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INFORMATION FOR SEQ ID NO: 4:
                                                                                                                                                                                                                                                                     APPLICANT: Peterson, Day
APPLICANT: Su, Xin-zhaun
APPLICANT: Wellems, Thom
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                                                                                                                                                                                                                                NUMBER OF SEQUENCES:
                                                                                                                                                                                                                                             TITLE OF INVENTION:
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APPLICATION NUMBER: PCT/AU90/00530
FILING DATE: 02-NOV-1989
ATTORNEY/AGENT INFORMATION:
NAME: Feeney, Joanne Longo
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   APPLICATION NUMBER: 1992062
FILING DATE: 1992062
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US/0
                                                                                                                                            STREET: 620 Newport Center Drive 16th Floor CITY: Newport Beach STATE: California
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                                                                                                                                       COUNTRY:
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Chitnis, Chetan
Miller, Louis H.
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SYSTEM: PC-DOS/MS-DOS
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Pred. No. 0.19;
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                                                                                                                                                                                                                                                        Patent No. 5670367
GENERAL INFORMATION:
                                                                                                                                                                                                                                                                      Sequence 14, Application US/08232463 Patent No. 5670367
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Best Local Similarity 47.3%;
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                COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
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INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                             APPLICANT: DORNER, F.
APPLICANT: SCHEIFLINGER,
APPLICANT: FALKNER, F. G
FILING DATE:
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                                                                                                                                                                                             NUMBER OF SEQUENCES:
                                                                                                                                                                                                      TITLE OF INVENTION:
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HYPOTHETICAL:
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TELECOMMUNICATION INFORMATION:
TELEPHONE: (619) 235-8550
         APPLICATION NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        122 ATTTTGTTGTGGAATGGAAGTAGTAATATACATTAAGCAAATTTTAAAAAAATTATATAAG 181
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ANTI-SENSE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ATTORNEY/AGENT INFORMATION:
NAME: Israelsen, Ned
                                                                                                       ZIP:
                                                                                                              COUNTRY:
                                                                                                                                        CITY: Alexandria
                                                                                                                                                      STREET:
                                                                                                                                                                  ADDRESSEE:
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1800 Diagonal Road,
                                                                                                               USA
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                                                                                                                                                                                                   RECOMBINANT FOWLPOX VIRUS
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        US/08/232,463
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Pred. No. 0.33;
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                                                                                                                                                  Suite 500
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CLASSIFICATION: 435

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Matches
                                                                                                                                      SOFTWARE:
SEQ ID NO 3
                                                                                                                                                                                                                                                                                                               Sequence 3, Application US/08213419B Patent No. 6333406 GENERAL INFORMATION:
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                                                                                                                                                                                   CURRENT APPLICATION NUMBER: US/08/213,419B
CURRENT FILING DATE: 1994-03-14
PRIOR APPLICATION NUMBER: US 07/870,506
PRIOR FILING DATE: 1992-04-17
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        REFERENCE/DOCKET NUMBER: 29,768
REFERENCE/DOCKET NUMBER: 3047:
TELECOMMUNICATION INFORMATION:
TELEPHONE: (703)836-9300
TELEFAX: (703)883-4109
TELEX: 899140
                                                                                                                                                                      NUMBER OF SEQ ID NOS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         INFORMATION FOR SEQ ID NO:
                                                                              TYPE: DNA ORGANISM: Plasmodium falciparum
                                       NAME/KEY: CDS
LOCATION: (24
                         NAME/KEY:
                                                                        FEATURE
                                                                                                                     ENGTH: 6124
                                                                                                                                                                                                                                                                                                                                                                                                                                   1226
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                   339
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            TOPOLOGY: 11
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         APPLICATION NUMBER: FILING DATE: 26-AUC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        APPLICATION NUMBER:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   AACTTTAAAATAAATAAAATTTGAGTAAATGTGTTTTCTGACTATTGAGGGGCAAAAAA 338
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CDS
(2598)..(3404)
                                                                                                                                                 PatentIn Ver. 2.0
                                   (2407)..(2439)
                                                                                                                                                                                                                                                                                 Inselburg, J. et al.
PENTION: GENE ENCODING PROTEIN ANTIGENS OF PLASMODIUM FALCIPARUM
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        7218 base pairs
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         4.0%; Score 44; DB ilarity 7.8%; Pred. No. 0.35; Conservative 138; Mismatches
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Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Matches 123;
                                                                TELEPHONE: 215-568-31
TELEFAX: 215-568-3439
INFORMATION FOR SEQ ID NO:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    GENERAL INFORMATION:
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LOCATION: (3850)..(5835)
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LOCATION: (3580)..(3720)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   APPLICANT:
APPLICANT:
                                                                                                    REFERENCE/DOCKET NUMBER: RITELECOMMUNICATION INFORMATION: 215-568-3100
                                                                                                                                                                                                                          PRIOR APPLICATION DATA:
APPLICATION NUMBER: AU PJ 7187
APPLICATION NUMBER: PCT/AU90/00530
                                                                                                                                                                                                                                                                                                              MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOTTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                     COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy
COMPUTER: IBM PC com
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                                                                                                                                                                        FILING DATE: 02-NOV-1989
ATTORNEY/AGENT INFORMATION:
NAME: Feeney, Joanne Lon
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             NUMBER OF SEQUENCES: 1
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  TITLE OF INVENTION:
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                                                                                                                                                      NAME: Feeney, Joanne Longo REGISTRATION NUMBER: 35,13
                                                                                                                                                                                                                                                                               APPLICATION NUMBER: FILING DATE: 199206
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STRANDEDNESS:
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Philadelphia
Philadelphia
                NUCLEIC
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: Chang, Andy C I
: Williams, Keit
                               5852 base pairs
                                                                                                                                                                                                                                                                                                                                                                                                                                          USA
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48.2%;
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Improved Plasmid Vectors for Cellular
Slime Moulds of the Genus Dictyostelium
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Pred. No. 0.37;
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TOPOLOGY: 1

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Best Local Similarity
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                             FILING DATE: 30-JAN-:
PRIOR APPLICATION DATA:
APPLICATION NUMBER:
                                                                                      PRIOR APPLICATION DATA:
APPLICATION NUMBER: WO 92/14818
FILING DATE: 12-FEB-1992
                                                                   APPLICATION NUMBER:
ATTORNEY/AGENT INFORMATION:
NAME: Saliwanchik, David
                                                                                                                                                                     SOFTWARE: Patentin Rel
CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                  COMPUTER READABLE FORM:
                                                                                                                                                                                                                                                                                                                                                                                                                     tent No.
                                                                                                                                                                                                                                                                                                                                                       TITLE OF INVENTION: NO. 54767
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            5826 TATTGTTACT 5835
                                                                                                                                                                                                                                                                                                                            CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                          NUMBER OF SEQUENCES:
                                                                                                                                                                                                                                                                                                                                                                    APPLICANT:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   APPLICATION NUMBER: US/07/991,867B
FILING DATE: 12-DEC-1992
CLASSIFICATION: 435
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    FILING DATE:
                                                                                                                                                                                             MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                         MEDIUM TYPE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     968 TATATTTTCT 977
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          848 AAAGGAGCATAACGAGGCAACAAAAGTAATGAACACGGAGAAACAAAAGCCATGAAGCTC 907
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                                                                                                                                                                                                                                                                                       Gainesville
                                                                                                                                                                                                                                                                                                                                                                                                                      2, Application US/07991867B
5476781
                                                                                                                                                                                                                                                                            Ξ
                                                                                                                                                                                                                                                                                           3: David R. Saliwanchik
2421 N.W. 41st Street, Suite A-1
                                                                                                                                                                             PatentIn Release #1.0, Version #1.25
                                                                                                                                                                                                                                                                USA
                                                                                                                                                                                                                                                                                                                                                                            Moyer, Richard W.
Hall, Richard L.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Conservative
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2378..5038
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2378..5038
                                                    UMBER: US 07/827,685
30-JAN-1992
                     JMBER: US 07/657,584
19-FEB-1991
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ö
                                                                                                                                                                                                                                                                                                                                        No. 5476781el Entomopoxvirus Expression System 66
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    DB 1;
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Best Local &
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                           1052 AAAGCCATTAGAAAGAGAAAGTGAGTGAGAGA 1083
448 GAGTTAAATATGGAATCAATACAAATAAAAGA 479
                                                388 TTAATAATATCTAAAAATAAATTTGGTAACTTTAATAATGTTTTTCCTATTAGTATAGTT 447
                                                                         992 CCCCTCTTACAAACAGAAGCTCCCTTTTTCAGTAGAAGTCCGATTCCCAATCTTAAAGAC 1051
                                                                                                                                 932 AAGATTTTATTAAATTTTAATGACGATGATAACAATTATATTTTCTGACTTCTTTAAAAC 991
                                                                                                                                                                                        872 AGTAATGAACACGGAGAAACAAAAGCCATGAAGCTCATTGGTTAGTTTAAGCTTAATAAG 931
                                                                                                                                                             268 TATAACAAAAATAGCAATATAAGTAATATTATACTACCACATTCTATAGAATTTTTAAAT 327
                                                                                                                                                                                                                   208 AATATTATTAAATTTAAATTTTATAACAAATTAAAAAATATAACATATTTAGATATATCT 267
                                                                                                                                                                                                                                              MOLECULE TYPE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              SEQUENCE CHARACTERISTICS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   REGISTRATION NUMBER: 31,794
REFERENCE/DOCKET NUMBER: UF
TELECOMMUNICATION INFORMATION:
TELEPHONE: 904-375-8100
                                                                                                                                                                                                                                                                                                    752 GATATTTATGATATAAATAGCTGTTAAACTATTTCAGCATCGCAGCTTTCTGCAACTTTT 811
                                                                                                                                                                                                                                                                                                                                                           692 ATGAAAGTTATAGTACTATTAGCCAGAGACAATTGATTATAGATATATCCATTAATCCAT 751
                                                                                                                                                                                                                                                                                                                                                                                                                                                                -991-867в-32
                                                                                                                                                                                                                                                                                                                                 TYPE: nucleic acid
STRANDEDNESS: double
TOPOLOGY: unknown
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              TELEFAX:
                                                                                                      TGTGAATCATGTAATATAAATGACTATAATTTAATTAATAATTTAGTAAATTTAAAAAAA 387
                                                                                                                                                                                                                                                                                                                                                                                                     174;
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                                                                                                                                                                                                                                                                                                                                                                                                   Conservative
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Pred. No. 0.29;
""smatches 218;
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                                                                                                                                                                                                                                                                                                                                                                                                                       Length 660;
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RESULT 15
US-08-107-755A-32
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Patent No. 5721352
GENERAL INFORMATION:
                                                                           COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
                                          SOFTWARE: Patentin Rel
CURRENT APPLICATION DATA:
                                                                                                                                                                                                          CORRESPONDENCE ADDRESS:
ADDRESSEE: David R. Saliwanchik
STREET: 2421 N.W. 41st Street, Suite A-1
                                                                                                                                                                                                                                                       APPLICANT: Moyer, Richard W.
APPLICANT: Hall, Richard L.
APPLICANT: Gruid1, Michael E.
TITLE OF INVENTION: No. 5721352el Entomopoxvirus Expression System
NUMBER OF SEQUENCES: 40
CLASSIFICATION:
                  FILING DATE:
                             APPLICATION NUMBER:
                                                                                                                                                                                          STATE:
                                                                                                                                                          ZIP:
                                                                                                                                                                      COUNTRY:
                                                                                                                                                       32606
                                                                                                                                                                                                       Gainesville
                                                                                                                                                                                                                                                                                                                                                                                  <sup>2</sup>, Application US/08107755A
5721352
                                                                                                                                                                                          Florida
                                                                                                                                                                                                                                                                                                       Moyer, kıc...
Hall, Richard L.
                                                                                                                                                                    U.S.A.
           19-AUG-1993
                         US/08/107,755A
                                                     Release #1.0, Version #1.25
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LENGTH: 660 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: double
; TOPOLOGY: unknown
; MOLECULE TYPE: DNA (genomic)
US-08-107-755A-32
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Search completed: March 30, 2003, 08:58:03 Job time: 183.503 secs
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APPLICATION UNMBER: US 07/827,658
ETLING DATE: 30-JAN-1992
PRIOR APPLICATION DATA:
APPLICATION DATA:
APPLICATION UNMBER: US 07/657,584
ETLING DATE: 19-FEB-1991
ATTORNEY/AGENT INFORMATION:
NAME: Saliwanchik, David R.
REGISTRATION NUMBER: 31/794
REFERENCE/DOCKET NUMBER: UF114.C2
TELECOMMUNICATION INFORMATION:
TELEPHONE: (904) 375-8100
INFORMATION FOR SEQ ID NO: 32:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Query Match 3.9%; Score 43.2; DB 1; Length 660; Best Local Similarity 44.4%; Pred. No. 0.29; Matches 174; Conservative 0; Mismatches 218; Indels 0;
                                                                                                       448 GAGTTAAATATGGAATCAATACAAATAAAAGA 479
                                                                                                                                                                                                                                                                                                              328
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OM nucleic - nucleic search, using sw model
                                                                                              GenCore version 5.1.4_p5_4578 Copyright (c) 1993 - 2003 Compugen Ltd.
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Run on: March 30, 2003, 08:25:26; Search time 83.8565 Seconds (without alignments) 11172.915 Million cell updates/sec

Title: Perfect score:

Sequence: US-09-502-426A-1\_COPY\_2102\_3202 1101 1 aatctacaaattattaatat.....gagagagagaaactagctcc 1101

Scoring table: IDENTITY\_NUC
Gapop 10.0 , Gapext 1.0

Searched: 574371 seqs, 425486471 residues

Total number of hits satisfying chosen parameters: 1148742

Minimum DB seq length: 0
Maximum DB seq length: 200000000

Post-processing: Minimum Match 0% Maximum Match 100% Listing first 45 summaries

Database 1: 2: 3: 3: 4: 3: 4: 5: 6: 7: 1: 110: 111: 113: 113: 114: Published\_Applications\_NA: \* /cgn2\_6/ptodata/1/pubpna/PCTUS\_PUBCOMB.seq:\*
/cgn2\_6/ptodata/1/pubpna/US08\_NEW\_PUB\_seq:\*
/cgn2\_6/ptodata/1/pubpna/US08\_NEW\_PUB\_seq:\*
/cgn2\_6/ptodata/1/pubpna/US09\_NEW\_PUB\_seq:\*
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/cgn2\_6/ptodata/1/pubpna/US10\_PUBCOMB.seq:\* /cgn2\_6/ptodata/1/pubpna/US07\_PUBCOMB.seq:\*
/cgn2\_6/ptodata/1/pubpna/PCT\_NEW\_PUB.seq:\*
/cgn2\_6/ptodata/1/pubpna/US06\_NEW\_PUB.seq:\*
/cgn2\_6/ptodata/1/pubpna/US06\_PUBCOMB.seq:\*
/cgn2\_6/ptodata/1/pubpna/US06\_PUBCOMB.seq:\*
/cgn2\_6/ptodata/1/pubpna/US06\_NEW\_PUB.seq:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

### SUMMARIES

c 19	c 18	c 17	c 16	c 15	C 14	c 13		11	c 10	. 9	0	c 7	ი 6	ი 5	c 4	c ω	2	c 1	Result No.
44	44.2	44.2	44.2	4.5	45.6	45.8	46	46.2	47	47.8	48.4	48.6	48.6	49.2	52.2	52.2	53.2	54.4	Score
4.0	4.0	4.0	4.0	4.1	4.1	4.2	4.2	4.2	4.3	4.3	4.4	4.4	4.4	4.5	4.7	4.7	4.8	4.9	Query Match
376	4187	4187	344	413	1109	428	32463	1713	419	294	406	53332	53332	6265	446	377	431	516	Query Match Length DB
10	10	9	10	10	9	10	9	9	10	10	10	10	9	10	10	10	10	10	BB
US-09-960-352-5087	US-09-764-855-252	US-10-072-349-252	US-09-960-352-1036	us-09-960-352-2919	US-09-938-842A-3333	US-09-960-352-573	US-09-996-956-5	US-09-938-842A-4756	us-09-960-352-11234	US-09-960-352-4637	US-09-960-352-10265	US-09-801-861-3	US-10-224-562-3	US-09-129-112-3	US-09-960-352-3400	US-09-960-352-7419	US-09-960-352-5558	US-09-960-352-5785	ID
5087	Sequence 252, App	Sequence 252, App	Sequence 1036, Ap	Sequence 2919, Ap	Sequence 3333, Ap	Sequence 573, App	Sequence 5, Appli	Sequence 4756, Ap	Sequence 11234, A	Sequence 4637, Ap	Sequence 10265, A	Sequence 3, Appli	Sequence 3, Appli	Sequence 3, Appli	Sequence 3400, Ap	Sequence 7419, Ap	Sequence 5558, Ap	Sequence 5785, Ap	Description

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US-09-938-842A-4902 US-09-938-842A-4902 US-09-754-853A-2	US-09-822-827-102 US-09-115-453-102	US-09-759-143-102 US-09-780-669-102 US-09-030-606-102	US-10-012-896-102 US-09-895-793-102 US-09-895-814-102	US-09-960-352-10262 US-09-232-880-102	US-09-803-719-1436 US-09-960-352-11218	US-09-790-988-1 US-09-960-352-7907 US-09-938-842A-4090	US-09-938-842A-3251 US-09-960-352-4582 US-09-938-842A-4975 US-09-938-842A-4975	US-09-754-853A-4 US-09-790-988-1 US-09-960-352-12911
Sequence 3089, Ap Sequence 4902, Ap Sequence 2, Appli		Sequence 102, App Sequence 102, App Sequence 102, App	Sequence 102, App Sequence 102, App Sequence 102, App	Sequence 937, App Sequence 10262, A Sequence 102, App	Sequence 1436, Ap Sequence 11218, A	Sequence 1, Appli Sequence 7907, Ap Sequence 4090. Ap	Sequence 3251, Ap Sequence 4582, Ap Sequence 4975, Ap	Sequence 4, Appli Sequence 1, Appli Sequence 12911

#### ALIGNMENTS

RESULT 1

Qy 65 AACAGAAACTTCCAAATTTTTTTTTTTTTATGGAACAAGAATAACAGATAGAAAACTATT 124	Query Match 4.9%; Score 54.4; DB 10; Length 516; Best Local Similarity 48.7%; Pred: No. 0.09; Matches 148; Conservative 0; Mismatches 156; Indels 0; Gaps 0;  TACARATTATTAGTTAGTCAATAACAATGCATAGAAAGTTCCAAAAAAAA	; ORGANISM: Bos taurus ; FEATURE: ; NAME/KEY: unsure ; LOCATION: (76),(90) ; OTHER INFORMATION: unsure at all n locations ; OTHER INFORMATION: Clone ID: 25-LIB3057-018-01-K1-G1 US-09-960-352-5785	APPLICANT: Tao, Nengbing APPLICANT: Byatt, John C. APPLICANT: Mathialagan, Nagappan TITLE OF INVENTION: NUCLEIC ACID AND OTHER MOLECULES ASSOCIATED WITH LACTATION AND TITLE OF INVENTION: MUSCLE AND FAT DEPOSITION FILE REFERENCE: 16511.006/37-21(10298)C CURRENT APPLICATION NUMBER: US/09/960,352 CURRENT FILING DATE: 2001-09-24 NUMBER OF SEQ ID NOS: 15112 SEQ ID NO 5785 LENGTH: 516 TYPE: DNA	US-09-960-352-5785/c ; Sequence 5785, Application US/09960352 ; Patent No. US20020137139A1 ; GENERAL INFORMATION: ; APPLICANT: Warren, Wesley C.
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                         RESULT 3
US-09-960-352-7419/c
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; ORGANISM: Bos taurus
; OTHER INFORMATION: Clone
US-09-960-352-5558
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US-09-960-352-5558/c
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Sequence 7419, Application US/09960352 Patent No. US20020137139A1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Query Match
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APPLICANT:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                APPLICANT: Byatt, John C.
APPLICANT: Mathialagan, Nagappan
TITLE OF INVENTION: NUCLEIC ACID AND OTHER MOLECULES ASSOCIATED WITH LACTATION AND
TITLE OF INVENTION: MUSCLE AND FAT DEPOSITION
FILE REFERENCE: 16511.006/37-21(10298)C
CURRENT EPPLICATION NUMBER: US/09/960,352
CURRENT FILING DATE: 2001-09-24
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            NUMBER OF SEQ ID NOS: 15112
SEQ ID NO 5558
LENGTH: 431
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                                                                                                                                                                                                                                                                                                                                                                                                              Match 4.8%;
Local Similarity 46.1%;
                                                                                                                                                                                                        CCAAATTTTTTTTTTTTTTTATGGAACAAGAAATAACAGATAGAAAACTATTTTGTTGTGGAA 135
                                                                                                                                                                                                                                                                                                                                                                                        CAAATTATAAATAAACCAACACGCTC
                                                                                                     TTCGGTAATAATCTAATAACTCTGTC 401
                                                                                                                                                       TCTGACTATTGAGGGGCAAAAAAAAGACAATGCCAAAAGTCTACGGGTTTGACTGTCCAG 375
                                                                                                                                                                                AAGTATGTTATCTAGTAGGTGTAATTAATAATGCATGGTGCGATTCAGAATTGGGACAAC 255
                                                                                                                                                                                                                                                                                                             TGGAAGTAGTAATATACATTAAGCAAATTTTAAAAAATTATATAAGCCTATACGCGCTCA 195
                                                                                                                               Tao, Nengbing
                                                                                                                                                                                                                                                                                                                                                                                                                                         Conservative
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GENERAL INFORMATION:

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; ORGANISM: Bos taurus
; OTHER INFORMATION: Clone ID: 32-LIB3057-025-Q1-K1-H11
US-09-960-352-7419

                                                                     US-09-960-352-3400
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SEQ ID NO 7419
LENGTH: 377
     Best Local Sin
Matches 165;
                                                                                                                                                                                                                                                                                                                                   GENERAL
                                                                                                                                                   SEQ ID NO 3400
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Best Local
                                                                                                                                                                 APPLICANT: Mathialagan, Nagappan
TITLE OF INVENTION: MUSCLEIC ACID AND OTHER MOLECULES ASSOCIATED WITH LACTATION
TITLE OF INVENTION: MUSCLE AND FAT DEPOSITION
FILE REFERENCE: 16511.006/37-21(10298)C
CURRENT FAPLICATION NUMBER: US/09/960,352
CURRENT FILLING DATE: 2001-09-24
NUMBER OF SEQ ID NOS: 15112
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                                                                                                                                                                                                                                                                               APPLICANT: Warren, APPLICANT: Tao, Ne APPLICANT: Byatt,
                                                                          LENGTH: 446
TYPE: DNA
ORGANISM: Bos taurus
OTHER INFORMATION: Clone ID: 15-LIB3058-052-Q1-K1-D11
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                870 AAAGTAATGAACACGGAGAAACAAA 894
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               GGATGAAAGTTATAGTACTATTAGCCAGAGACAATTGATTATAGATATATCCATTAATCC 749
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 INFORMATION:
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   Conservative
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                                                                                                                                                                                                                                                                                                                   Wesley C.
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                  46.78;
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 Score 52.2; Di
Pred. No. 0.23
0; Mismatches
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                    . 23;
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     188;
   Indels
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Best Local S
Matches 173
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SOFTWARE: PatentIn Ver. 2.1
SEQ ID NO 3
LENGTH: 6265
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                                                                                                                                                                                                                                                                                                                                                                               APPLICANT: Etzler, Marilynn E.
APPLICANT: Murphy, Judith B.
APPLICANT: The Regents of the University of California
TITLE OF INVENTION: A No. US20020019995A1 Factor Binding Protein From Legume Roots
FILE REFERENCE: 023070-079810US
CURRENT APPLICATION UNDER: US/09/129,112
CURRENT FILING DATE: 1998-08-04
PRIOR APPLICATION UNDER: US 08/907,226
PRIOR FILING DATE: 1997-08-06
                                                                                                                                                        NAME/KEY: exon
LOCATION: (169
2877 TCTTTTTTTTTTTTTTTTTATTGAAAATGTTTTGAAATATTGTCAAATATTAATAATAGTGA 2818
                                                                                                                                                                                                                                                                              NAME/KEY: exon
LOCATION: (633)..(944)
                                          2936 TATTTTATACTGTTTTACTATTCAAATAAACATAATGCAGATATGAAGTTTACTG-AACT 2878
                                                                                                                                                                                                                                                                                                OTHER INFORMATION: genomic sequence of NBP46
                                                                                                                                                                                                                                                                                                                        ORGANISM: Dolichos biflorus
                                                                                                                                                                                                                                                    NAME/KEY: exon
                                                                                                                                                                                                                                                          LOCATION: (945)..(1022)
               hes 173;
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Similarity 53.1%;
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                                                                                                                                                                                          (1560)..(1616)
                                                                                                                                                                                                                 (1152)..(1559)
                                                                                                                                                                                                                                      (1023)..(1151)
                                                                                              Conservative
                                                                                       Score 49.2; DB 10;
Pred. No. 2.4;
0; Mismatches 148;
                                                                                        Indels
                                                                                                            Length 6265;
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Sequence 3, Application US/09801861
Patent No. US20020119544A1
GENERAL INFORMATION:
APPLICANT: YAN, Chunhua et al.
TITLE OF INVENTION: ISOLATED HUMAN
TITLE OF INVENTION: ACID MOLECULES
TITLE OF INVENTION: THEREOF
                                                                                                             RESULT 7
US-09-801-861-3/c
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US-10-224-562-3
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FILE REFERENCE:
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TITLE OF INVENTION: ISOLATED HUMAN KINASE PROTEINS, NUCLEIC
TITLE OF INVENTION: ACID MOLECULES ENCODING HUMAN KINASE PROTEINS, AND USES
TITLE OF INVENTION: THEREOF
FILE REFERENCE: CL001098DIV
CURRENT APPLICATION NUMBER: US/10/224,562
CURRENT APPLICATION NUMBER: US/10/224,562
NUMBER OF SEQ ID NOS: 10
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Sequence 3, Application US/10224562 Publication No. US20030022229A1 GENERAL INFORMATION:
                                                                                                                                                                31431 AATATATAAATATAAATATAT 31409
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                                                                                                                                                                                 287 AATAAATAAAAATTTGAGTAAAT 309
                                                                                                                                                                                                                                                                                                                     167
                                                                                                                                                                                                                                                                                                                                                         107 AACAGATAGAAAACTATTTTGTTGTGGAATGGAAGTAGTAATATACATTAAGCAAATTTT 166
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                                                                                                                                                                                                                                                                                                                                                                                                             311 TGTTTTCTGACTATTGAGGGGCAAAA 336
                                                                                                                                                                                                                                         TGCATGGTGCGATTCAGAATTGGGACAACAATGAAAACGGAATTAAAATATTAACTTTAA 286
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 YAN, Chunhua et al.
WENTION: ISOLATED HUMAN KINASE PROTEINS, NUCLEIC
WENTION: ACID MOLECULES ENCODING HUMAN KINASE PROTEINS, AND USES
                                                                                                                                                                                                                                                                                                                                                                                                                                                           Conservative
CL001098
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49.0%; Pred. No. 7;
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CURRENT APPLICATION NUMBER: US/09/801,861
CURRENT FILING DATE: 2001-03-09
NUMBER OF SEQ ID NOS: 10

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; OTHER INFORMATION: Clone ID: 44-LIB3058-038-Q1-K1-C12
US-09-960-352-10265
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; ORGANISM: Human
US-09-801-861-3
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                                                                                                                                                                                                                                                   SEQ ID NO 10265
LENGTH: 406
                                                                                                                                                             Query Match
Best Local
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                                                                                                                                                                                                                                                                                                                                                                                                                 Sequence 10265, Application US/09960352 Patent No. US20020137139A1
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Best Local Similarity
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SEQ ID NO 3
                                                                                                                                                                                                                                                                                                       APPLICANT: Byatt, John C.

APPLICANT: Mathialagan, Nagappan

TITLE OF INVENTION: NUCLEIC ACID AND OTHER MOLECULES ASSOCIATED WITH LACTATION AND FITTLE OF INVENTION: MUSCLE AND FAT DEPOSITION

FILE REFERENCE: 16511.006/37-21(10298)C
                                                                                                                                                                                                                                                                           CURRENT APPLICATION NUMBER: US/09/960,352
CURRENT FILING DATE: 2001-09-24
NUMBER OF SEQ ID NOS: 15112
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155
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                                                                                                                       Local Similarity
                                                               AAACTATTTTGTTGTGGAATGGAAGTAGTAATACATTAAGCAAATTTTAAAAAAATTAT 176
                                                                                                ATTTTTTTTATTTTAAATTAIGTGTTTCATTTTAGTATTTATATTAAATTATTCCTTAA
                        AATAAATAAAATTTGAGTAAAT
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                                                                                                                                                             Score 48.4;
Pred. No. 1.
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Pred. No. 7
                                                                                                                                                 Mismatches
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                                                                                                                                                   Indels
                                                                                                                                                                         Length 406;
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; OTHER INFORMATION: Clone US-09-960-352-11234
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; OTHER INFORMATION: Clone ID: 20-LIB3058-054-Q1-K1-E11
US-09-960-352-4637
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                                                                APPLICANT: Tao, Nengbing
APPLICANT: Byatt, John C.
APPLICANT: Byatt, John C.
APPLICANT: Byatt, John C.
APPLICANT: Mathalagan, Nagappan
TITLE OF INVENTION: NUCLEIC ACID AND OTHER MOLECULES ASSOCIATED WITH LACTATION /
TITLE OF INVENTION: MUSCLE AND FAT DEPOSITION
FILE REFERENCE: 16511.006/37-21(10298)C
CURRENT APPLICATION NUMBER: US/09/960,3552
CURRENT APPLICATION NUMBER: US/09/960,3552
CURRENT FILING DATE: 2001-09-24
NUMBER OF SEQ ID NOS: 15112
SEQ ID NO 11334
LENGTH: 419
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                                                                                                                                                                                                                                                                                                           Sequence 11234, Application Patent No. US20020137139A1
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LENGTH: 294
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APPLICANT: Byatt, John C.
APPLICANT: Byatt, John C.
APPLICANT: Byatt, John C.
APPLICANT: Mathalagan, Nagappan
TITLE OF INVENTION: NUCLEIC ACID AND OTHER MOLECULES ASSOCIATED WITH LACTATION AND FITE REPERENCE: 16511.006/37-21(10298)C
CURRENT APPLICATION NUMBER: US/09/960,352
CURRENT FILING DATE: 2001-09-24
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            NUMBER OF SEQ ID NOS: 15112
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                                 ORGANISM: Bos taurus
                                                  TYPE: DNA
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mes 115; Conserv
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               ID: 48-LIB3058-052-Q1-K1-D8
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Pred. No. 1.4;
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; ORGANISM: Arabidopsis thaliana
US-09-938-842A-4756
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Best Local Similarity
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                                                                                                                                                                                                                                                                                                                                                                                                                                                  GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                             Sequence 4756, Application Patent No. US20020160378A1
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CURRENT APPLICATION NUMBER: US/09/938,842A
CURRENT FILING DATE: 2001-08-24
PRIOR APPLICATION NUMBER: US 60/227,866
PRIOR FILING DATE: 2000-08-24
                                                                                                                                                                                                                                                               PRIOR APPLICATION NUMBER: US 60/264,647
PRIOR FILING DATE: 2001-01-16
PRIOR APPLICATION NUMBER: US 60/300,111
PRIOR FILING DATE: 2001-06-22
                                                                                                                                                                                                                                                                                                                                                                          TITLE OF INVENTION: STRESS-REGULATED GENES OF PLANTS, TRANSGENIC PLANTS CONTAINING TITLE OF INVENTION: SAME, AND METHODS OF USE
                                                                                                                                                                                                                                                                                                                                                                                                            APPLICANT: Harper, Jeff
APPLICANT: Kreps, Joel
APPLICANT: Wang, Xun
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                                                                                                                                                                                                                               LENGTH: 1713
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                                                                  111 GATAGAAAACTATTTTGTTGTGGAATGGAAGTAGTAATATACATTAAGCAAATTTTAAAA 170
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                                                                                                          71 AACTTCCAAATTTTTTTTTTTTTTTATGGAACAAGAAATAACAGATAGAAAACTATTTTGTTG 130
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                                                                                                                                            Conservative
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Pred. No. 5.7;
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; TYPE: DNA
; ORGANISM: Homo sapiens
US-09-996-956-5
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Best Local Similarity
Matches 142; Conserv
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SEQ ID NO 5
LENGTH: 32463
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                                                                                                                                                                                                                                                                       Sequence 573, Application US/09960352 Patent No. US20020137139A1
                                                                                                                                                                                                                                                  GENERAL INFORMATION:
                    APPLICANT: Byatt, John G.
APPLICANT: Mathialagan, Nagappan
TITLE OF INVENTION: NUCLEIC ACID AND OTHER MOLECULES
TITLE OF INVENTION: MUSCLE AND FAT DEPOSITION
FILE REFERENCE: 15511.006/37-21(10298)C
CURRENT APPLICATION NUMBER: US/09/960,352
CURRENT FILING DATE: 2001-09-24
                                                                                                                                              APPLICANT: Warren, Wesley
APPLICANT: Tao, Nengbing
APPLICANT: Byatt, John C.
APPLICANT: Mathialagan, N
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CURRENT FILING DATE: 2001-11-30
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  NUMBER OF
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SEQ ID NOS:
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ilarity 47.08;
Conservative
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Pred. No.
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CURRENT APPLICATION NUMBER: US/09/938,842A
CURRENT FILING DATE: 2001-08-24
F PRIOR APPLICATION NUMBER: US 60/227,866
PRIOR FILING DATE: 2000-08-24
PRIOR APPLICATION NUMBER: US 60/264,647
PRIOR FILING DATE: 2001-01-16
PRIOR APPLICATION NUMBER: US 60/300,111
PRIOR APPLICATION NUMBER: US 60/300,111
PRIOR FILING DATE: 2001-06-22
NUMBER OF SEQ ID NOS: 5379
SEQ ID NO 3333
FEDETAL TONA
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US-09-938-842A-3333/c
US-09-938-842A-3333/c
; Sequence 3333, Application
; Patent NO. US20020160378A1
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                                                                                                             Matches
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LENGTH: 428
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                                                                                                                                                                                                                                                                                                                                                                                       APPLICANT: Wang, Xun
APPLICANT: Zhu, Tong
TITLE OF INVENTION: STRESS-REGULATED GENES OF PLANTS, TRANSGENIC PLANTS CONTAINING
TITLE OF INVENTION: SAME, AND METHODS OF USE
FILE REFERENCE: SCRIP1300-3
                                                                                                                                                                                                                                                                                                                                                                                                                                                                   APPLICANT: Harper, Jeff
APPLICANT: Kreps, Joel
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OTHER INFORMATION: Clone ID: 03-LIB3058-031-Q1-K1-A11
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                                                                                                                          Local Similarity
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Pred. No. 6.
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; NUMBER OF SEQ ID NOS: 15112

; SEQ ID NO 2919

; LENGTH: 413

; TYPE: DNA

; ORGANISM: Bos taurus

; OTHER INFORMATION: Clone ID: 13-LIB3058-032-Q1-K1-D1

US-09-960-352-2919
Search completed: March Job time: 210.856 secs
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APPLICANT: Warren, Wesley C.
APPLICANT: Tao, Nengbing
APPLICANT: Byatt, John C.
APPLICANT: Byatt, John C.
APPLICANT: Byatt, John C.
APPLICANT: Mathialagan, Nagappan
TITLE OF INVENTION: NUCLEIC ACID AND OTHER MOLECULES ASSOCIATED WITH LACTATION INTITLE OF INVENTION: MUSCLE AND FAT DEPOSITION
FILE REFERENCE: 16511.006/37-21(10298)C
CURRENT APPLICATION NUMBER: US/09/980,352
CURRENT FILING DATE: 2001-09-24
NUMBER OF SEQ ID NOS: 15112
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Best Local Similarity
Matches 138; Conserv
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                                                                                                                                                                                                                                                                                                            483 TTAATATTAATGAATAGTTCATAT 460
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#### REFERENCE AUTHORS SOURCE ORGANISM ACCESSION VERSION LOCUS DEFINITION RESULT 1 BH811044/c COMMENT KEYWORDS TITLE JOURNAL BH811044.1 GSS. Contact: Joseph R. Ecker Salk Institute Genomic Analysis Laboratory (SIGnAL) The Salk Institute for Biological Studies 10010 N. Torrey Pines Road, La Jolla, CA 92037, USA Tel: 858 453 4100 x1752 Fax: 858 558 6379 Alonso,J.M., Leisse,T.J., Barajas,P., Chen,H., Cheuk,R.,,C., Jeske,A., Karnes,M., Kim,C.J., Parker,H., Prednis,L., Zimmerman,J. and Ecker,J.R. A Sequence-Indexed Library of Insertion Mutations in the Arabidopsis thaliana Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; Rosidae; eurosids II; Brassicales; Brassicaceae; Arabidopsis. BH811044 148 bp DNA linear GSS 02-MAY-2002 SALK\_057128 Arabidopsis thaliana TDNA insertion lines Arabidopsis thaliana genomic clone SALK\_057128, DNA sequence. Arabidopsis Genome Unpublished (2001) thale cress. вн811044 This is single pass sequence recovered from the left border of (bases 1 to 148) ecker@salk.edu GI:20388862 Prednis,L., Cheuk, R., Gadrinab Shinn, P

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JOURNAL
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                                                                                                                         Submitted (17-JUN-2002) Weisshaar B., Max-Planck-Institut fuer 2 uechtungsforschung, Carl-von-Linne-Weg 10, Koeln, 50829, Germany This sequence is recovered from the left border of the T-DNA. It indicates an insertion within the locus defined by clone T3A5. The sequences are generated at the MPI for Plant Breeding Research in the context of the GABI-Kat project, GABI-Kat is part of the Grman Plant Genomics program designated 'GABI'. Information on line
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Rosso,M., Strizhov,N., L1,Y., Reiss,B., Dekker,K. and Weisshaar,B. A new Arabidopsis thaliana T-DNA mutagenised population (GABI-Kat) for flanking sequence tag based reverse genetics
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Arabidopsis thaliana
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
Rosidae; eurosids II; Brassicales; Brassicaceae; Arabidopsis.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            AL768954 473 bp DNA linear GSS 18-JUN Arabidopsis thaliana T-DNA flanking sequence GK-082A08-011867,
                                                              availability can be found at: http://www.mpiz-koeln.mpg.de/GABI-Kat/.
                                                                                                                                                                                                                                                                                                                                                                                   \text{Li,Y.}, \text{Rosso,M.}, \text{Strizhov,N.} and \text{Weisshaar,B.} Direct Submission
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Unpublished
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Strizhov, N., Li, Y., ROSSO, M., Viehoever, P., Dekker, K., Saedler, H
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AL768954.1 GI:21522073
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Unpublished
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         A pipeline for automated high-throughput generation of FSTs (flanking sequence tags) from Arabidopsis thaliana T-DNA
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/clone="ish=K.057128"
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/clone="ish=K.057128"
/clone="ish=N.057128"

                         Location/Qualifiers
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Pred. No.
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6.6e-18;
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                                                                 - Web: www.genoscope.cns.fr)

Determination of this BAC-end sequence was carried out as part of a collaboration with the Berkeley Drosophila Genome Project (BDGP). The BDGP is constructing a physical map of the Drosophila melanogaster genome using these BACs. For further information please see http://www.fruitfly.org The BDGP Drosophila melanogaster BAC library was prepared by Kazutoyo Osoegawa and Aaron Mammoser in Pleter de Jong's laboratory in the Department of Cancer Genetics at the Roswell Park Cancer Institute in Buffalo, NY. The library is named RPCI-98 and was constructed by partial EcoRI digestion of Drosophila DNA provided by the BDGP from the isogenic strain y2; cn bw sp, the same strain used for the BDGP's Pl and EST libraries. A more detailed description of the library
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          CCCT 473
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                                                                                                                                                                                                                                                                                                                                                                                    Submitted (02-JUN-1999) Genoscope - Centre National de Sequencage BP 191 91006 EVRY cedex - FRANCE (E-mail : segref@genoscope.cns.fr | Web : www.genoscope.cns.fr |
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Drosophila melanogaster.
Drosophila melanogaster
Drosophila melanogaster
Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;
Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha;
Ephydroidea; Drosophilidae; Drosophila.
and how to order individual BAC clones, the entire library, or filters for hybridization from the BACPAC Resource Center can be found at http://bacpac.med.buffalo.edu/drosophila_bac.htm.
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BACROBKIO of RPCI-98 library from
fly), genomic survey sequence.
AL063921
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/clone_lib="Arabidopsis thaliana T-DNA insertion lines"
/note="PCR was performed on DNA from Arabidopsis thaliana
plants (T1) which were transformed with the T-DNA from
vector pAC161. The lines contain one or more T-DNA
insertions. The DNA fragment(s) resulting from the PCR
were directly sequenced to determine the genomic sequence
flanking the insertion. Sequences displaying significant
similarity to the A. thalaina nuclear genome sequence were
processed for submission. T-DNA derived sequences were
removed"
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Pred. No. 1.3e-17;
0; Mismatches 24
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                                                                                                                                                                                                                                                                                                                                                                                                                                                          СМТМНИННИМНЕННИАСНАННЕТ НИСМСНИЕМИСТ СНЕНЕТМУ НИТ СНЕМИНЕМНЕНИН
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                                                                                                                    Drosophila melanogaster.

Drosophila melanogaster

Drosophila melanogaster

Eukaryota, Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;

Eukaryota, Metazoa; Arthropoda; Brachycera; Muscomorpha;

Reoptera; Endopterygota; Diptera; Brachycera; Muscomorpha;

Ephydroidea; Drosophilidae; Drosophila.
                                                                                                                                                                                                                                       CNS0167M 1201 bp
Drosophila melanogaster genome sur
BACN15M24 of DrosBAC library from
fly), genomic survey sequence.
AL106396
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97; Conserv
 Submitted (23-JUL-1999) Genoscope - Centre BP 191 91006 EVRY cedex - FRANCE (E-mail: - Web: www.genoscope.cns.fr)
Determination of this BAC-end sequence was collaboration with the European Drosophila
                                                                                               Genoscope
                                                                                 Direct Submission
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/db_xref="taxon:7227"
/clone="BaCR08K10"
/clone_lib="RPCI=98"
/note="end : TET3"
a 64 c 131 g
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19.2%;
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Pred. No. 0.00
18; Mismatches
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survey sequence T7 end of BAC
rom Drosophila melanogaster (fruit
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(E-mail :
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                                               National de Sequencage
segref@genoscope.cns.fr
Genome Project
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ACCESSION VERSION KEYWORDS

AL071865

SOURCE ORGANISM

Drosophila melanogaster. AL071865.1 GI:4948170

REFERENCE

Ephydroidea;

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928)

Drosophila melanogaster Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygo Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha; Ephydroidea; Drosophilidae; Drosophila.

Pterygota;

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RESULT 5
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                                                                                                                                                                                                                                                                                                                                                        200;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   http://www.edgp.ebi.ac.uk -. This Drosophila melanogaster BAC library (Dros BAC) was made by Alain Billaud at CEPH (Centre d'Etude du Polymorphisme Humain) with funding provided by a MRC project grant. The DNA was prepared from embryos by Alain Bucheton and Genevieve Payan. It has been constructed in the vector
          Drosophila melanogaster genome sur
BACR27A24 of RPCI-98 library from
                                       CNSOODKY
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genomic survey sequence
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/note="end : T7"
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/clone_lib="DrosBAC"
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/db_xref="taxon:7227"
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TITLE
                                                           ORGANISM
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Best Local
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  please see http://www.fruitfly.org The BDGP Drosophila melanogaster BAC library was prepared by Kazutoyo Osoegawa and Aaron Mammoser in Pieter de Jong's laboratory in the Department of Cancer Genetics at the Roswell Park Cancer Institute in Buffalo, NY. The library is named RPCI-98 and was constructed by partial EcoRI digestion of Drosophila DNA provided by the BDGP from the 1sogenic strain y2; on bw sp. the same strain used for the BDGP's Pl and EST libraries. A more detailed description of the library and how to order individual BAC clones, the entire library, or filters for hybridization from the BACPAC Resource Center can be found at http://bacpac.med.buffalo.edu/drosophila_bac.htm.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Web: www.genoscope.cns.fr)
Determination of this BAC-end sequence was carried out as pari
collaboration with the Berkeley Drosophila Genome Project (BDO
The BDGP is constructing a physical map of the Drosophila
melanogaster genome using these BACs. For further information
Drosophila melanogaster
Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;
Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha;
Ephydroidea; Drosophilidae; Drosophila.
                                                                                                                                                                 Drosophila melanogaster genome survey sequence SP6 end of BACN15C02 of DrosBAC library from Drosophila melanogaster
                                                                                                                                                                                                         CNS0165X
                                                                           Drosophila melanogaster.
                                                                                                               AL106335.1 GI:5621422
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Direct Submission
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/note="end : T7"
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/db_xref="taxon:7227"
/clone="BACR27A24"
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                                                                          Drosophila melanogaster
Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;
Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha;
Ephydroidea; Drosophilidae; Drosophila.
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AL061936
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Determination of this BAC-end sequence was carried out as part of collaboration with the European Drosophila Genome Project (EDGP) - http://www.edgp.ebi.ac.uk - This Drosophila melanogaster BAC library (Dros BAC) was made by Alain Billaud at CEPH (Centre d'Etude du Polymorphisme Humain) with funding provided by a MRC project grant. The DNA was prepared from embryos by Alain Bucheton and Genevieve Payan. It has been constructed in the vector
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BP 191 91006 EVRY cedex
                                  Direct Submission
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/plasmid="pBeloBAC11"
/note="end : SP6"
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/db_xref="taxon:7227"
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segref@genoscope.cns.fr
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Drosophila melanogaster
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Eukaryota, Metazoa; Arthropoda; Brachycera; Muscomorpha;
Rephydroidea; Drosophilidae; Drosophila.
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/db_xref="taxon:7227"
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                                        TTAATAAGAAGATTTTATTAAATTTTAATGACGATGATAACAATTATATTTTCTGA
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Locustian melanogaster
Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;
Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha;
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- Web : www.genoscope.cns.fr)
Determination of this BAC-end sequence was carried out as part of collaboration with the Berkeley Drosophila Genome Project (BDGP). The BDGP is constructing a physical map of the Drosophila constructing a physical map of the Drosophila recommendation of the BDGP is constructing a physical map of the Drosophila constructing a physical map of the Drosophila recommendation of the BDGP is constructed by the BDGP is const
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                                                                                                                                           AAGCCATGAAGCTCATTGGTTAGTTTAAGCTTAATAAGAAGATTTTATTAAATTTTAATG 953
                                                                                                                                                                                                   KRRKKKRAAAKKKBRKKTGRKGRRKGGRARKKGRGAARGAAGRRKKNKKGDAWATTTTD
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/clone_lib="G"
/note="Genoscope sequence ID : C0AG225BH02LP1-end : T7"
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Score 63.6; Pred. No. 0. Mismatches

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Length 1146; Indels

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Submitted (12-APR-2000)
This sequence is a single read and was generated as scale clone-end sequencing project of the Tetraodon genome. For more information, please take a look at http://www.genoscope.cns.fr/Tetraodon.
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Human gene number estimate provided by genome wide analysis using Tetraodon nigroviridis DNA sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Charaterization and repeat analysis of the compact genome of the freshwater pufferfish Tetraodon nigroviridis
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Roest-Crollius, H., Jaillon, O., Dasilva, C., Fizames, C., Fisher, Bouneau, L., Billault, A., Quetier, F., Saurin, W., Bernot, A. and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Tetraodon nigroviridis.
Tetraodon nigroviridis.
Tetraodon nigroviridis.
Eukaryota, Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Actinopterygii; Neopterygii; Teleostei; Euteleostei; Neoteleostei;
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1 (bases 1 to 1146)
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                                                                                                                                                                                                                                                                                                                                                                      Submission
/organism="Tetraodon nigroviridis"
/db_xref="taxon:99883"
/clone="225004"
                                                                                                                                                    Location/Qualifiers
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CNS0021J/c
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Determination of this BAC-end sequence was carried out as part of a collaboration with the Berkeley Drosophila Genome Project (BDGP). The BDGP is constructing a physical map of the Drosophila melanogaster genome using these BACs. For further information please see http://www.fruitfly.org The BDGP Drosophila melanogaster BAC library was prepared by Kazutoyo Osoegawa and Maron Mammoser in Pieter de Jong's laboratory in the Department of Cancer Genetics at the Roswell Park Cancer Institute in Buffalo, NY. The library is named RPCI-98 and was constructed by partial EcoRI digestion of Drosophila DNA provided by the BDGP from the isogenic strain y2; cn bw sp, the same strain used for the BDGP's Pl and EST libraries. A more detailed description of the library
                                                                                                                                                                                                                    TITTTTTWTTAWATTAAAAWATAAWAWATWTTTATTAAATTTWTTATAAAATTAAAA 564
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Drosophila melanogaster genome survey sequence TET3 end of BAC #BACR05N11 of RPCI-98 library from Drosophila melanogaster (fruitfly), genomic survey sequence.
                                                            Drosophila melanogaster genome sur
BACR24D09 of RPCI-98 library from
                                                                                                            CNS00BO1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 and how to order individual BAC clones, the entire library, or filters for hybridization from the BACPAC Resource Center can be found at http://bacpac.med.buffalo.edu/drosophila_bac.htm.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Submitted (02-JUN-1999) Genoscope - Centre National de Sequencage
BP 191 91006 EVRY cedex - FRANCE (E-mail : seqref@genoscope.cns.fr
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                    fly), genomic survey sequence.
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Ephydroidea; Drosophilidae;.Drosophila.
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/note="end : TET3"
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/db_xref="taxon:7227"
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49.2%;
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rom Drosophila melanogaster
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                                                              TGACTTCT 984
                                                                                                          AATAAWTSTAMAATSVCASBSSVWTTATATTTTTTASAAAWAWAKAWAATTTTSTGSTRT
                                                                                                                                   TTTAAGCTTAATAAGAAGATTTTATTAAAATTTTAATGACGATGATAACAATTATATTTTC 976
                                                                                                                                                                                                                                       TAACGAGGCAACAAAAGTAATGAACACGGAGAAACAAAAGCCATGAAGCTCATTGGTTAG
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Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha;
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Location/Qualifiers
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/db_xref="taxon:7227"
/clone="BACR24D09"
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/note="end : T7"
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                                                                                                                                                                                                                                                                                                                                                                                 Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           AL Submitted (02-dUN-1999) Genoscope - Centre National de Sequencage : BP 191 91006 EVRY cedex - FRANCE (E-mail : seqref@genoscope.cns.fr)
- Web : www.genoscope.cns.fr)
- Determination of this BAC-end sequence was carried out as part of a collaboration with the Berkeley Drosophila Genome Project (BDGP).

The BDGP is constructing a physical map of the Drosophila melanogaster genome using these BAGs. For further information please see http://www.fruitfly.org The BDGP Drosophila melanogaster BAC library was prepared by Kazutoyo Osoegawa and Aaron Mammoser in Pieter de Jong's laboratory in the Department of Cancer Genetics at the Roswell Park Cancer Institute in Buffalo, NY. The library is named RPCI-98 and was constructed by partial EcoRI digestion of Drosophila DNA provided by the BDGP from the isogenic strain y2; cn bw sp, the same strain used for the BDGP's Pl and EST libraries. A more detailed description of the library and how to order individual BAC clones, the entire library, or filters for hybridization from the BACPAC Resource Center can be received.
                                                                                                                                                                                                                                                                                                                                     TWATWWAATAAATTTTWT
                          TGAGTAAATGTGTTTTCT 318
                                                                                                                                                   TATTTTGTTGTGGAATGGAAGTAGTAATATACATTAAGCAAATTTTAAAAAATTATATAA 180
                                                                                                                                                                                                                                            TGTTAACAGAAACTTCCAAATTTTTTTTTTTTTATGGAACAAGAAATAACAGATAGAAAAC 120
                                                          CNSUUD87 1009 bp DNA linear GSS 03-JUN-1999 Drosophila melanogaster genome survey sequence TET3 end of BAC # BACR1N01 of RPCI-98 library from Drosophila melanogaster (fruit
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Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha;
Ephydroidea; Drosophilidae; Drosophila.
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/clone-"BACR11N01"
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Determination of this BAC-end sequence was carried out as part of a collaboration with the Berkeley Drosophila Genome Project (BDGP). The BDGP is constructing a physical map of the Drosophila melanogaster genome using these BACs. For further information please see http://www.fruitfly.org The BDGP Drosophila melanogaster BAC library was prepared by Kazutoyo Osoegawa and Aaron Mammoser in Pieter de Jong's laboratory in the Department of Cancer Genetics at the Roswell Park Cancer Institute in Buffalo, NY. The library is named RPCI-98 and was constructed by partial ECORI digestion of Drosophila DNA provided by the BDGP from the 1sogenic strain y2; on bw sp, the same strain used for the BDGP's and how to order individual BAC clones, the entire library or filters for hybridization from the BACPAC Resource Center can be found at http://bacpac.med.buffalo.edu/drosophila_bac.htm.
ATGTGTTTTCTGACTATTGAGGGGCAAAAAAAAAAGACAATGCCAAAAGTCTACGGGTTTGA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       AAATTATTAATATTTAGTCAATAACAATGCATAGAAAGTTCCAAAAAAATTTTGTTAAC 67
                                                                                WTTWTAWWATWWAWWTATAWATAWAATAWAWAWAWATAAATAWATAWATWAAAWAWA
                                                                                                                                                                                                                                                          CGCGCTCAAAGTATGTTATCTAGTAGGTGTAATTAATAATGCATGGTGCGATTCAGAATT
                                                                                                                                                                                                                                                                                                                  TTGTGGAATGGAAGTAGTAATATACATTAAGCAAATTTTAAAAAATTATATAAGCCTATA 187
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         AGAAACTTCCAAATTTTTTTTTTTTTATGGAACAAGAAATAACAGATAGAAAACTATTTTG 127
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Submitted (02-JUN-1999) Genoscope - Centre National de Sequencage : BP 191 91006 EVRY cedex - FRANCE (E-mail : seqref@genoscope.cns.fr
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Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha;
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/note="end : T7"
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/db_xref="taxon:7227"
/clone="BACR29B23"
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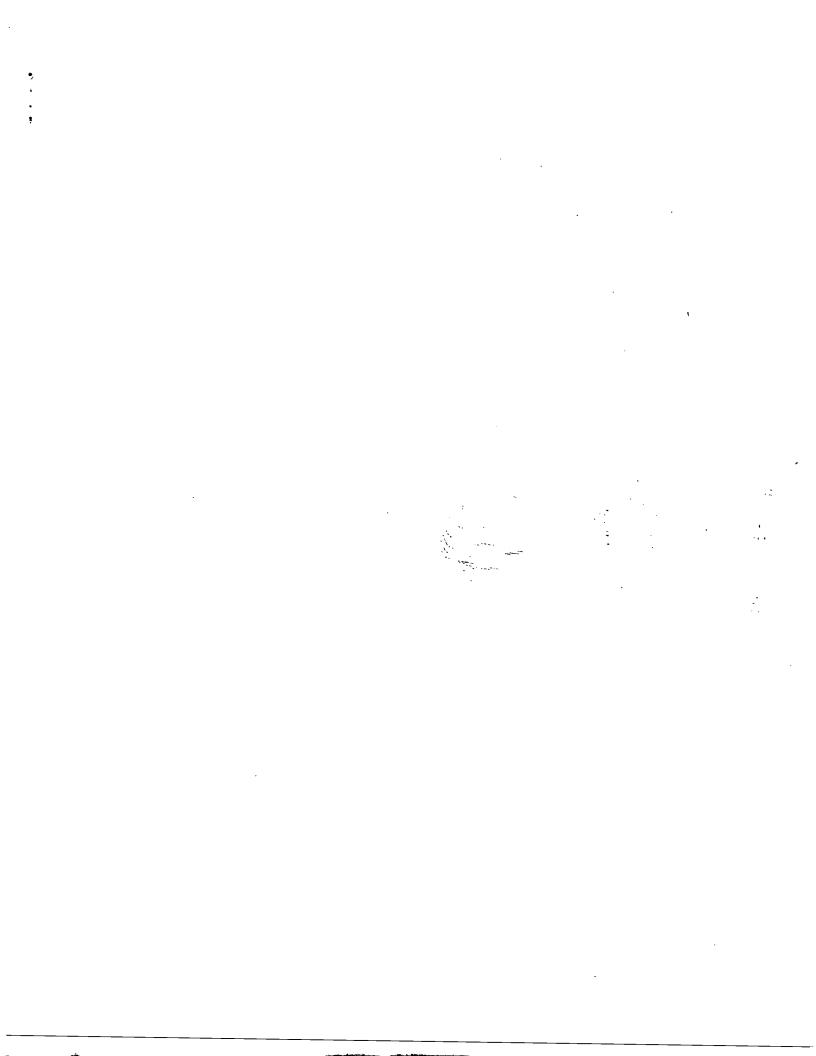
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                                       186 TACGCGCTCAAAGTATGTTATCTAGTAGGTGTAATTAATAATGCATGGTGCGATTCAGAA 245
                                                                               591 ATAAATTAWAAAAWAWAAAAAAAAWATTTTATATTTWTTAAATTTAAAANATNANANATA 650
                                                                                                                                                                 531 ЖААТТААТИТТАААТТАЛАТЖТТТТАЛАЛАЛАЛАМИТАЛАМАЛАЛАЛАЛАЛАЛАЛАЛАЛА 590
                                                                                                                                                                                                                                                / Match 5.7%; Score 62.4; DB 17; Length 855; Local Similarity 44.0%; Pred. No. 0.038; nes 153; Conservative 18; Mismatches 177; Indels. 0;
                                                                                                                                                                                                                                                                        368 CTGTCCAGTTCGGTAATAATCTAATAACTCTGTCTTTGA 406
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                                                                                                                                                                                             ACAGAAACTICCAAATTITTTTTTTTTATGGAACAAGAATAACAGATAGAAAACTATTT 125
                                                                                                                         TGTTGTGGAATGGAAGTAATATATACATTAAGCAAATTTTAAAAAATTATATAAAGCCTA 185
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            This sequence is a single read and was generated as part of a large scale clone-end sequencing project of the Tetraodon nigroviridis genome. For more information, please take a look at http://www.genoscope.cns.fr/Tetraodon.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Direct Submission
Submitted (12-APR-2000)
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Charaterization and repeat analysis of the compact genome of the
freshwater pufferfish Tetraodon nigroviridis
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Roest-Crollius, H., Jaillon, O., Dasilva, C., Fizames, C., Fisher, C., Bouneau, L., Billault, A., Quetier, F., Saurin, W., Bernot, A. and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Roest-Crollius,H., Jaillon,O., Dasilva,C., Bouneau,L., Fisher,C., Bernot,A., Fizames,C., Wincker,P., Brottier,P., Quetier,F., Saurin,W. and Weissenbach,J.
Human gene number estimate provided by genome wide analysis using Tetracdon nigroviridis DNA sequence
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Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Actinopterygii; Neopterygii; Teleostei; Euteleostei; Neoteleostei;
Acanthomorpha; Acanthopterygii; Percomorpha; Tetraodontiformes;
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Qγ
                   В
              AAATGTGTTTTCTGACTATTGAGGGGCAAAAAAAAGACAATGCCAAAA 353
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Search completed: March 30, Job time: 1451.66 secs 2003, 08:52:57

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GenCore version 5.1.4_p5_4578 Copyright (c) 1993 - 2003 Compugen Ltd.
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Post-processing: Minimum Match 0% Maximum Match 100% Listing first 45 summaries Title: Perfect score: Run OM nucleic -Database Minimum Scoring table: Sequence: Total number of hits satisfying chosen parameters: Maximum on: 멂 seq seq nucleic search, using sw model length: 0 length: 2000000000 US-09-502-426A-1\_COPY\_1\_3202 3202 IDENTITY\_NUC
Gapop 10.0 , Gapext 1.0 1 atgtgggtattatattgttg.....gagagagagagaactagctcc 3202 March 29, 2054640 seqs, 14551402878 residues GenEmbl: \* gb\_pr:\* gb\_pat:\* gb\_ph:\* gb\_pl:\* gb\_htg:\*
gb\_in:\* em\_htg\_hum:\*
em\_htg\_inv:\*
em\_htg\_other:\*
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em\_htg\_rod:\*
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em\_htgo\_mus: \* b\_om:\* 2003, 18:06:10 ; Search time 31531.6 Seconds (without alignments) 2955.362 Million cell updates/sec 4109280

Pred. No. is the number of results predicted by chance ៥ have a

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score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

### SUMMARIES

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AC011458 AL807813 AC104069 AC098822 AC097483 AC069525 AC127383 AC011355 AC12778	AC11/444 AC069435 AB083339 AB070264 AC096750 HS1108D11	10407 MAL1P T3A5 73185 73185 73185 10542 102088 12088 12088 12738	C1208 FMAL3 C1054 MU115 MU375 FMAL1 MU115 C0695	ATT3A5 AF044216 ALB44732 AC005504 AC004157 AC004157 AC004159 AC004159 AC093899 PFMAL3P5	ID
ACU011458 Homo sapi AL807813 Human DNA AC104069 Homo sapi AC098822 Homo sapi AC007483 Homo sapi AC069525 Homo sapi AC127383 Homo sapi AC011355 Homo sapi AC126178 Homo sapi	11/44 HOMO Sap 069435 HOMO Sap 083339 Bombyx m 070264 Bombyx m 096750 Homo sap 034419 Human DN	073 Homo sap 746 Plasmodi 746 Plasmodi 959 Arabidop 959 Human DN 425 Homo sap 425 Homo sap 963 Homo sap 973 Homo sap 369 Homo sap 269 Homo sap	83 Homo 56 Plasr 25 Homo Drosopl Drosopl Drosopl Drosopl Drosopl Drosopl Drosopl Drosopl	5891515429	tion

#### ALIGNMENTS

RESULT 1
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DEFINITION
ACCESSION
VERSION SOURCE ORGANISM REFERENCE KEYWORDS AUTHORS

Arabidopsis thaliana DNA chromosome AL132979 AL132979.2 GI:6782244 84196 bp DNA e 3, linear PI BAC clone T3A5. PLN 26-JAN-2000

Arabidopsis thaliana. Arabidopsis thaliana Arabidopsis thaliana Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnollophyta; eudicotyledons; core eudicots; Rosidae; eurosids II; Brassicales; Brassicaceae; Arabidopsis. 1 (bases 1 to 84196)
Bloecker, H., Mewes, H.W.,
Salanoubat, M. Lemcke, K., Mayer, K.F.X., Quetier, F. and

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JOURNAL
REFERENCE
AUTHORS
TITLE
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Submitted (25-JAN-2000) MIPS, at the Max-Planck-Institut fuer Submitted (25-JAN-2000) MIPS, at the Max-Planck-Institut fuer Biochemite, Am Klopferspitz 18a, D-82152 Martinsried, FRG, E-mai Lenckeemips, blochem.mpg dee, mayeremips, blochem.mpg de Project Coordinator: Marcel Salanoubat and Francis Quetier, Groupement d'Interet Public, Centre National de Sequencage - GENOSCOPE; 2 Gaston Cremieux, BP191, 91006 Evry Cedex, France;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              On Jan 27, 2000 this sequence version replaced g1:6434247.
Information on performance of analysis and a more detailed annotation of this entry and other sequences of chromosomes 3, 4 and 5 can be viewed at: http://www.mips.blochem.mpg.de/proj/thal/.
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RYKGYDIPSGWKVLPVISAVHLDNSRYDQPNLENPWRRQONNGASSGSGSFSTWGN
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QVADTR"
                  complement(28289.
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                                             ATATGAGTAAATCAAAAAGAGTATTGAATTGAAGTGTAAACATATTTCGTTATGACCCCCA 360
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ilarity 99.5%;
Conservative
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Complement (38307. 38796)
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complement(40243. .40336)
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40180. .40242,40337. .40401,40489. .40564,40655. .40734,
40805. .40919,41225. .41323))
/note="Contains Eukaryotic putative RNA-binding region RNP-1 signature AA179-186"
/codon_start=1
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/gene="T3A5.50"
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1500	Db 30761 CTTGGATTCCATTCAATGATCTAAAATGCATAGATCTTTTGGGTTACAGTTTCGAAGTCC 1
1440 30762	1311 ATATCATTCTTGGTTGGTCAACAATAAAAACA 30821 ATATCATTCTTGGTTGGTCAACAATAAAAACA 30821 ATATCATTCTTGGTTGGTCAACAATAAAAAACA
1380 30822	30881 GATAAATCACACGCGTGGTAATAATTATGGGACCGTATGTTACGATCACTGCAA 30881 GATAAATGAAATTCACACGCGTGGTAATAATTATGGGACCGTATGTTACGATCACTGCAA
1320 30882	GGTATGCTATACCTTCACGTATGCTATACTAGAGACTAAAGAATAGTTATGTGATGTC
1260 30942	T-201 ACATATACATAATTCCTTACAGAAAAAACAAACTTAAGAGAAGTTAACATATCCATATAT
1200 31002	31061 CCGGTTGTTATGTAAAT 31061 CCGGTTGTTATGTAAAT
1140 31062	UGI TATTTATACAA
1080 31122	31181 CGATTTTACAGCGTCA
1020 31182	31240 ACCATTTTGAAACA 31240 ACCATTTTGAATCA 3127 ACCATTTTGAATAACATTTTTTTTCAAACA 3127 ACCATTTTAAACATTTTTTTTTTAAACA
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TATCCTAAGGGTAATTTTGGAAATCCCCAATTTAAACCGATTGAGACCGTACCGGACTTCC
                     TAGGGGTCCTTCTGACATTTTCACTGTTCTACCCCTACTCGTGAGCCCACCCTTTTCCCA
                                                   GGGTTTGACTGTCCAGTTCGGTAATAATCTAATAACTCTGTCTTTGACCGCACGCTCGTG
                                                                                TAAATACATTATGAACCAATAATAGTTGGTGAATTCAAATATCTCCATTAATATTTTTTG
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                                           GGGTTTGACTGTCCAGTTCGGTAATAATCTAATAACTCTGTCTTTGACCGCACGCTCGTG
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                  Submitted (22-JAN-1998) Plant Tucson, AZ 85721, USA
                                      Choe, S., Dilkes, B
Direct Submission
                                                                                                           The DWF4 gene of Arabidopsis encodes a mediates multiple 22alpha-hydroxylation
                                                                                                                                 Choe, S., Dilk, Feldmann, K.A.
                                                                                                                                                     Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; Rosidae; eurosids II; Brassicales; Brassicaceae; Arabidopsis.

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                AATAACTCTGTCTTTGACCGCACGCTCGTGTAGGGGTCCTTCTGACATTTTCACTGTTCT 2550
                                                                            GGCAAAAAAAAAGACAATGCCAAAAGTCTACGGGTTTTGACTGTCCAGTTCGGGTAATAATCT
                                                                                                                                                                                                                                              TAAAATATTAACTTTAAAATAAATAAAAATTTGAGTAAATGTGTTTTCTGACTATTGAGG
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                                                           GGCAAAAAAAAGACAATGCCAAAAGTCTACGGGTTTGACTGTCCAGTTCGGTAATAATCT
                                                                                                                                                                                     GTAGGTGTAATTAATAATGCATGGTGCGATTCAGAATTGGGACAACAATGAAAACGGAAT
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/product="steroid 22-alpha-hydroxylase"
/protein_id="AACO5093.1"
/db_xxef="gi:293542"
/db_xxef="gi:293542"
/translation="METEHHTLLPLLLLPSILLSLLLFLILLKRRNRKTRFNLPPGKS
GWPFLGETICYLKPYTATTLGDFWQOHVSKYGKIYRSNLFGEPTIVSADAGLNRFILQ
NEGRLFECSYPRSIGGILGKWSMLVLVGDMHRDMRSISINFLSHARLFTILLKDVERH
TLFVLDSWQONSIFSAQDEAKKTFFNLMKHIMSMDGEEETFGLKKEYVTFMKGVVS
APLNLPGTAYHKALGSRATILKFIERKMEERKLDIKEEDQEEEEVKTEDEAEMSKSDH
VRKORTDDDLLGWVLKHSNLSTEQIILDILLSLLFAGHETSSVAIALAIFTLQACPKAV
EELREHLEIARAKKELGESELNWDDYKKMDFTCQVINETLALGNVVRFLHRKALKDV
RYKOYDIPSGWKVLPVISAVHILDNSRYDQPNLFNWRWQQQNNGASSGSGSSSTWGN
NYMPFGGGPRLCAGSELAKLEMAVFIHHLVLKFNWELAEDDQPFAFPFVDFPNGLPIR
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/note="member of the cytochrome P450 superfamily; CYP90B1"
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join(1133. 1353,1434. 1758,1844. 1996,2095.
2562. 2654,2746. 2824,2931. 3040,3795. 404
/gene="DWF4"
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2562. <u>2654,</u>2746. .2824,2931. .3040,3795. .4398)
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/chromosome="III"
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/strain="Ws-2"
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                                                                                                                                            AAAGTAATGAACACGGAGAAACAAAAGCCATGAAGCTCATTGGTTAGTTTAAGCTTAATA
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JOURNAL REFERENCE AUTHORS JOURNAL Unpublished Murphy, G (bases

1 to 191)

Clarke, J.H.,

Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; Rosidae; eurosids II; Brassicales; Brassicaceae; Arabidopsis.

., Bowles,B., Carter,J., Hart,D., McCullagh,B., Langham,S., LeGrys,C., Jones,J.D.G. and Bevan,

Bevan, M.

Arabidopsis thaliana. Arabidopsis thaliana

STS; STS, sequence tagged site

AL844732.1 GI:21998461

tagged site. AL844732

Arabidopsis thaliana transposon

191 đđ

insertion DNA

linear STS 25-JUL-2002 STS SM\_3.29533, sequence

AL844732

Clarke, J.H.

Direct Submission

Submitted (25-JUL-2002) Clarke J.H., John Innes Centre, Colney Lane, Norwich, NR4 7UJ, UK

AT denotes an activation tag dissociation transposon within a single line, ET an enhancer trap dissociation transposon, GT a grap dissociation transposon, MT a mis-expression enhancer trap dissociation transposon, MS a defective suppressor mutator transposon. 3 denotes a sequence derived from the 3'end of the transposon, \_5 denotes a sequence derived from the 5'end of the gene

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                                                                                                                          94304, USA
On Apr 2, 1999 this sequence version replaced gi:4337172.
* NOTE: This is a 'working draft' sequence. It currently
* consists of 3 contigs. The true order of the pieces
* is not known and their order in this sequence record is
* arbitrary. Gaps between the contigs are represented as
* runs of N, but the exact size of the fanished sequence
* This record will be updated with the finished sequence
* as soon as it is available and the accession number will
* be preserved.
                                                                                                                                                                                                                                                                                                                   2 (bases 1 to 104992)
Hyman, R.W., Qin, F., Fung, E.L., Conway, A.B. and Davis, R.W.
Direct Submission
Submitted (21-AUG-1998) Stanford DNA Sequencing and Technology
Center, Stanford University, 855 California Avenue, Palo Alto,
                                                                                                                                                                                                                                                                                                                                                                                                                                                    Plasmodium falciparum
Eukaryota; Alveolata; Apicomplexa; Haemosporida; Plasmodium.
1 (bases 1 to 104992)
Hyman,R.W., Fung,E.L., Qin,F., Tamaki,T., Kurdi,O.B., Conway
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AC005504.3 GI:4558584
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Plasmodium falciparum chromosome 12,
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seed stock requests: http://nasc.nott.ac.uk/ NASC stock
Location/Qualifiers
1. .104992
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/db_xref="taxon:3702"
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                               58642: contig of 58642 bp in length
58842: gap of unknown length
91011: contig of 32169 bp in length
91211: gap of unknown length
104992: contig of 13781 bp in length
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Pred. No. 3.8e-16;
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Best Local Similarity 44.7
Matches 1041; Conservative
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CTCGACCCTTAAAATACGATTTTACAGCGTCACTAGTTGAGATTACTAGCATAAAGCATA 1064
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                                                         AAAACAATTGTCTGGGACCATTTTGAATAAACTTTTTCTCAAACATTACGGGACACTGGA 1004
                                                                                     TTTGTTTCGTTTCTCTTAACTATATTATCGCGGATATATGATAACAATGATATCAC 944
                                                                                                                                                                                                      ATGAATTATTTAAATAATTAAAACAATAATATATATATAATTAATTATATTTAGTAAAT 73165
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/db_xref-"taxon:5833"
/chromosome-"12"
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Pred. No. 1.7
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1.7e-10;
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                 2061 AATAGTTGGTGAATTCAAATATCTCCCATTAAT----ATTTTTTGAAATCTACAAATTATT 2116
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                                                                                                                                                                                                                                                                                                                                                                                                                                                              TTTCCTATGTTCTTAAAATATTTTTTTTTTATATTTAGTTATAAATACATTATGAACCAAT
                                                                       AATTTTTGAAAAATGTTATAAATTTCTAACAATATTATTAAAATATGATGCCTATAATGTA 2000
                                                                                                             AATTCAATGCTACTATCAATAGAAGAAACAGCTGAGTATTACATTTTAATTTAAAGACAA 1940
                                                                                                                                                 ATAATGACAGCCTCTACAACTGTGATAGTCAATTT---TTTCTGCAAATATTAAATTAGG
                                                                                                                                                                                                       TAATTTAATTAATAATATATATATATATTTATATTATTTGTTTAATATTTAATTACTATT 7418:
                                                                                                                                                                                                                                           GAGGTAAAAA--AAGTTTTGTCTTATTTTCGCGATGCATGAAGGATAAACCTAATGACTT 1763
                                                                                                                                                                                                                                                              ACATACTTTGGATGTTTAAACTTAATCTTGTTTCTTCCTACGGTATAAATATTAATCATC
                                                                                                                                                                                                                                                                                                  TGTAACATTA-----CAATATTTATATTAGATACTAGTATGTGATTATTCCAAAT 1645
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Best Local Similarity
Matches 1041; Conserv
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                108 ATAATTAAATATTAAAAATTCATTTAAAAATATTTACA-AGTAATTAATTATCTTTACATTG 166
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               AATATTTAGTCAATAACAATGCATAGAAAGTTCCAAAAAAATTTTGTTAACAGAAACTT 2176
                                                                                                                                                                                                                                                                                                                                                                               On Aug 12, 2000 this sequence version replaced gi:8810447
* NOTE: This is a 'working draft' sequence. It currently
* consists of 2 contigs. The true order of the pieces
* is not known and their order in this sequence record is
                                                                                                                                                                                                                                                                                                                                                                                                                                                         Submitted (19-FEB-1998) Stanford DNA Sequencing and Technology Center, Stanford University, 855 California Avenue, Palo Alto,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Hyman, R.W., Fung, E.L., Qin, F., Rowley, D., Kurdi, O.B., Conway, A.B. and Davis, R.W. Plasmodium falciparum 3D7 chromosome 12
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    2 (bases 1 to 169546)
Hyman,R.W., Qin,F., Fung,E.L., Conway,A.B. and Davis,R.W.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Unpublished
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Eukaryota; Alveolata; Apicomplexa; Haemosporida; Plasmodium.
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                                                                                                                                                                                                                                                                                                               arbitrary. Gaps between the contigs are represented as runs of N, but the exact sizes of the gaps are unknown. This record will be updated with the finished sequence as soon as it is available and the accession number will be preserved.
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                                                                     Conservative
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23667
                                                                                                                                                               /clone="PFYAC293"
/clone="3D7"
                                                                                                                                                                                       /organism="Plasmodium
/db_xref="taxon:5833"
/chromosome="12"
                                                                                                                                                                                                                                     1. .16954
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44.78;
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23666: gap of unknown length
169546: contig of 145880 bp in length
                                                             Score 133.2; DB 2;
Pred. No. 1.5e-10;
0; Mismatches 1248;
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	1295	TAACATATCCATATATGGGTATGCTATACCTTTCACGTATGCTATACTAGA	1245	Qy
	85167	ATAAATAAACAATAATTAAATTAATATATATATAATAATA	85108	망
	1244	AGAGAAGT	1185	δÃ
	85107		85048	망
	1184	ATGTT	1125	Qγ
	1124 85047	AAGGACCCGTTCAAGCTATTTATACAAAGTTACAAACTGAATATAGCTTGAAATCCTTTA	1065 84988	р. О
	1064 84987	CTCGACCCTTAAAATACGATTTTACAGCGTCACTAGTTGAGATTACTAGCATAAAGCATA	1005 84928	D Q
	1004 84927	AAAACAATTGTCTGGGACCATTTTGAATAAACTTTTTCTCAAACATTACGGGACACTGGA	945 84870	p Q
•	944 84869	TTTGTTTCGTTTCTCTTAACTATATATATCGCGGATATATGATAACAATGATATATCAC	<b>1</b> 8	p &
	884 84809	TCAATATTATGTTCCAGGTATTTGCATAATCTTCTGTTTAAAGCATATTTTGTCTTTCTT	825 84750	₿ <b>%</b>
	824 84749	TGGATATTCGTTAAAATTTGCGATAACGATTGTGAAAAATATTTTATTTGTTAGCTGATC	765 84690	4d 5d
	764 84689	TGGAATAATGGTCCCTGCCAGCTTTCTCTCACAATCAATATCGACCCTATTTGGATTTTC	705 84633	gg VQ
	704 84632	TGACCCATGGAGTATGTGAATAATTATCAAAGAGAATAAGAGTGACCAAAGGTTG	645 84573	д <b>у</b>
	644 84572	CAGCAAATTATTAACAAGAGTATTGAGAAAAAACCGAAAATAAGAAAAGGGAAAGAGTAG	585 84513	₽ 2
	584 84512	ACGAGTGTGAATATCCGTTTATCGATCACTCCAATCATGATTATGATTCTTGTGCTAATC	525 84453	р 8
	524 84452	ATGAAGATTTTCTTACCAATTAAAATTTCGAATTCATATCTCTTGATTAATTA	465 84393	B 6
	464 84392	TTTTTGGTTCTGGATTAGGTTTATTTGATCATACTACATGCATCATTTCTTTGATTACT	405 84333	g S
	404 84332	TCGTTATGACCCCCAAAAAAAAAAAAAAAACAAACA - AACAAACCCCCCCC	346 84273	р 8
	345 84272	TCTTTTGTTATATGTATATGAGTAAATCAAAAAGAGTAFTGATTGAAGTGTAAACATATT	286 84213	β δ
	285 84212	AATAATAAAGGAAATAATCGATTCCATTTGGTTGGAT-TACACAGTTAAGTTTTTGTGTT	227 84153	₽ 2
	226 84152	TATTGTTATAACAAAATATCTATCTTTGGTATATGGAGAAAATATGGAGTTTGGAATTTAT	167 84093	B &

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                                   74559 AAAATAAAAATAATAATTATTATTATATATATATATTAATTAAATTAAATTAAATTATTAT 74500
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TAATAATAAAGGAAATAATCGATTCCATTTGGTTGGATTACACAGTTAAGTTTTTGTGTT
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Submitted (21-AUG-1998) Stanford DNA Sequencing and Technology
Center, Stanford University, 855 California Avenue, Palo Alto,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       AC005504 104992 bp Di
Plasmodium falciparum chromosome 12,
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* NOTE: This is a "working draft' sequence. It currently consists of 3 contigs. The true order of the pieces is not known and their order in this sequence record is arbitrary. Gaps between the contigs are represented as runs of N, but the exact sizes of the gaps are unknown. This record will be updated with the finished sequence as soon as it is available and the accession number will be preserved.
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                                                                                                                                                                                                                                                                                                                                                                                                                       /organism="Plasmodium falciparum"
/db_xref="taxon:5833"
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58842: gap of unknown length
91011: contig of 32169 bp in length
91211: gap of unknown length
104992: contig of 13781 bp in length
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                                                                                                                                                                                                                                                                                                                     Score 130.8; DB 2; Pred. No. 3.8e-10;
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2, *** SEQUENCING IN PROGRESS
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Eukaryota; Alveolata; Apicomplexa; Haemosporida; Plasmodium. 1 (bases 1 to 165546)

Hyman,R.W., Fung,E.L., Qin,F., Rowley,D., Mao,J., Tamaki,T., Kurdi,O.B., Conway,A.B. and Davis,R.W.

Plasmodium falciparum 3D7 chromosome 12
                                                               Plasmodium falciparum
                                                                                                   AC004157.8 GI:9797712
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Plasmodium falciparum chromosome 12 clone
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Best Local Similarity 44.38;
GAGTAGTGACCCATGGAGTATGTGAATAATTATCAAAGAGAATAAGAGAGATGACAACCAAA
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Hyman,R.W., Qin,F., Fung,E.L., Conway,A.B. and Davis,R.W.
Direct Submission
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23666: gap of unknown length
169546: contig of 145880 bp in length
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                                                                                      GCGAACTTGTAACATTACAATATTTATATTAGATACTAGTATGTGATTATTCCAAATACA
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Direct Submission
Submitted (02-NOV-1998) The Institute for Genomic
Wadical Center Drive, Rockville, MD 20814, USA
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2 (bases 1 to 14867)

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Science 282
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complement(1570.
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                                                                                                       /chromosome="2
                                                                                                                                    /db_xref="taxon:36329"
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MEYCTLIKKGKYDDMTIYKLKEVIKATHHILCDKTKHLETFOSDIDYSTLLNSLNNK
FILNKIIDKNFILFYECLLKILLNIKFVNFQSLCISLISKNITYNILRNNVIIVNNV
LFNDIKKFSLYLCNIFIGKRIKTENENAVLIHNNDOTNYSNKENIKDIIJOKRIKEY
IFYKMENYKDFHFKLKDSDLLSIKLLSNTFVKINEVYNSYDFYLLFNNISCILYNFLV
NRNSVKKYKDTYIYILNDLSFYYKJIKNDRTKKKNFFLLSSSMKEBLICKNILSVSN
RYIKHLHEEDNFDQKDQYVCSLTFLNNLFFDKIIFFHYIYNLMCHVYKTYNVFKCNKL
INEDIISLLLLTCSKFQYFIENNSNDRYCRKELHLKYNIIDDLIKNYLNTYNSSISID
NISKIFISLSNSKYTCEVNENLLLESLQSEFEKVTKTSKKGGIHMMDNNLLDNNNSCE
KYEHRYIEYKKENLFINLNKIIBCLIKLNIFIYLKKKKTYLLYLYKGSLCPINLKENII
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HEIYKLLFIFNKYLNNNSNIPFNKNLIQEMEFNLYYFREIKNEKNYIIKMNKKEIYKK
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/SIFSKKRDSHKGSSFKRFTSKRKSGSFKKPYYROKILKNYNNYKGRUFINGR
DNFKGRFGSFCSRYEDINKGSFKKRFISKRNKSVKSYKGKROKSHKMGKKSEKKRAFINGR
TVVTKRLNNYKTVSAPVKKFNNLNISLYRKNRTFALNTKRSKPVGTIKSSVPRKRIKK
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NNVKLNYEKSNNSNGNISNILKDDKNKNHNNVEMDLIDNKNENKKIQEKGQNGENCEN
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TNKKIYKKSKAQSLFDKGLNIHDKLILFKNLPKYKCAKYECISAKEVYKYLLDEYKKC
FNY SICDIIQSVKIFDELDKTFTDYNFYIEVKNIDKNVLNKINEIYFKNKDITFHRR
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/protein_id="AAC71888.
/db_xref="GI:3845199"
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/note="predicted by
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/codon_start=1
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Submitted (12-JUN-2002) Department of Genetics, Washington Submitted (12-JUN-2002) Department of Genetics, Missouri 6: University, 4444 Forest Park Avenue, St. Louis, Missouri 6: On Feb 5, 2002 this sequence version replaced gi:15625013.
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Submitted (05-FEB-2002) Genome
University School of Medicine,
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Direct Submission
Submitted (10-SEP-2001) Genome
University School of Medicine,
MO 63108, USA
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NOTICE: This sequence may not represent the entire insert of this clone. It may be shorter because we only sequence overlapping clone sections once, or longer because we provide a small overlap between neighboring data submissions.

all regions were double stranded, sequenced with an alternate chemistry, or covered by high quality data (i.e., phred quality >-30); an attempt was made to resolve all sequencing problems, such as compressions and repeats; all regions were covered by sequence from more than one subclone; and the assembly was confirmed by restriction This sequence was finished as follows unless otherwise noted:

# MAPPING INFORMATION:

Mapping information for this clone was provided by Dr. John D. McPherson, Department of Genetics, Washington University, St. MO. For additional information about the map position of this sequence, see http://genome.wustl.edu/gsc b. Louis

## SOURCE INFORMATION:

The RPCI-11 human BAC library was made from the blood of one male donor, as described by Oscegawa, K., Woon, P.Y., Zhao, B., Frengen, E. Tateno, M., Catanese, J.J. and de Jong, P.J. (1998) An improved approach for construction of bacterial artificial chromosome libraries. Genomics 51:1-8. The clone may be obtained either from Research Genetics, Inc. (http://www.resgen.com) or Pieter de Jong and coworkers at http://www.chori.org pBACe3.6

1

ORGANISM

Homo sapiens

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

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NEIGHBORING SEQUENCE INFORMATION:
Actual start of this clone is at base at base position 172816 position 1 of RP11-724016; of RP11-724016.

Unresolved simple 25900. sequence repeat from base position

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SOURCE ORGANISM KEYWORDS

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AUTHORS

PPMAL395
Plasmodium falciparum MAL395, complete sequence.
AL034556 AL008971 AL008972 AL008978 AL010141 AL010153 AL010162
AL010206 AL010210 AL139179
AL010266 AL010210 AL139179
AL034556.3 GI:7711064
HTG: centromere; CTRP protein; initiation factor E4;
Serine/threonine protein phosphatase.
Plasmodium falciparum 3D7
Plasmodium falciparum 3D7
Eukaryota; Alveolata; Apicomplexa; Haemosporida; Plasmodium.
1 (bases 1 to 86877)
Bowman, S., Lawson, D. Basham n. Brown D. Chilliannach T.

Bowman, S., Lawson, D. Basham n. Brown D. Chilliannach T.

Bowman, S., Lawson, D. Basham n. Brown D. Chilliannach T.

Bowman, S., Lawson, D. Basham n. Brown D. Chilliannach T.

Bowman, S., Lawson, D. Basham n. Brown D. Chilliannach T. Bowman,S., Lawson,D., Basham,D., Brown,D., Chillingworth,T., Churcher,C.M., Craig,A., Davies,R.M., Devlin,K., Feltwell,T. Gentles,S., Gwilliam,R., Hamlin,N., Harris,D., Holroyd,S., Feltwell, T., 04-MAY-2000

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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            On or before May 14, 2001 this sequence version replaced g1:2982535, g1:2982536, g1:2894454, g1:2982554, g1:2982562, g1:2894489, g1:2982572, g1:2982574, g1:4493931. For more information about this sequence or the Malaria Project,
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Unpublished
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Bowman, S., Skelton, J.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              falciparum
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Location/Qualifiers
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                                                                                                                                                                                       (revised 1024. .10
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Join(242. ..., MAL3P5.1"
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complement(3354..6644)
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                                                                                                                                                                                                                                                                                  816.
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FTMKLNIERNNKNIIRSNYDNINNDISIDKOMYMMNE IDVNINISIDEXIKEOPENF
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/note="predicted splice donor
PFC0575w (revised)"
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ISNNEINIIKLKKLNQSDEDINLTSDLIYERLRTKVLWYIQKIEYLKFKYQYDIINEQ
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(revised of PFC0575w)"
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/note="predicted splice do
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                                                                                                                                                                                                                                                                                                     (revised)
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)575w, MAL3P5.1"
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(MAL3P5.2),
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ii,M.A.,
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prc0581w"
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LKYKDEIVSKKNNFSFSALSNDSNSYKKITVTHTHIFFIKTSTKRASYGKVVV
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QNFLKEEKNNSDKLQDDIDEDEEKYFDEEILREAKKKSEEYDKDDEEL"
7790. .7799
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FDKDNKIIYLMSADYMNNLRRNILKRPSKNEBRENINSFASFPFLLSKNIIYFEDEIG
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NNNNICSNNNNNICSNNNNNICSNKMLDEFQDNKFNDYNTKKEKRK
YFLKNIKTTNNIFDYLKGKKEKHQNEDNTINLYYIKKKFPMIFYLKNIKKNDTSFIEH
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YFLKMMEHINEKLYKMKRAFHYYIYNEDQFIINNYYHIIHKKNIHKHHHLKQCKDKE
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hexExon"
/note="potential
PFC0581w"
                                                                                                /note="potential splice PFC0581w"
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/note="poten+1=1
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8302. .8686.8568. .8641,8713. .8812,8924. .9006,9122.
9369. .9505,9613. .9838)
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LYTQRIQNCCDIFSYIYKKYNFNEKNPFLNYLYYELHYIVYSEKKKKKKFFSFISSSP
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LFKYIYSFFFFKKEENHIYDLFEDQMMNHLHKKENDKFYNYSNENTHNNIYKYISDNY
FYDHINSSSNRCSFKNLKKQQTDDNTKHIIMGKEKYPMNKSDHEKKNNNTCGNINIEK
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KRREAIKYNFISDEQNLFNRFYEYFIYEFYSIKYGILSPHLSUFILKNISEHCYNIYP
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                                                                                                                                              /gene="PFC0581w"
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                                                'gene="PFC0581w"
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CCCGATATAGTTTTTGGTTCTGGATTAGGTTTATTTGATCATAATTACATGCATCATTTC
                                                                      GTTTTTGTGTTTTCTTTTTGTTATATGTATATGAAGTAAATCAAAAAAGAGTATTGAATTGAAGT
                                                                                                         ATCTTTACATTGTATTGTTATAACAAAATATCTATCTTTGGTATATGAGAAAATATGGAG
                                                                                                                                                                                            Conservative
                                                                                                                                                                                                                                                                                                         /note="potential
PFC0581w"
                                                                                                                                                                                                                                                                                                                           'gene="PFC0581w"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           /note="potential splice
PFC0581w"
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/note="potential splice acceptor sequence for
PFC0581w"
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/note="potential
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Pred. No. 1.1e-09;
0; Mismatches 1307;
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Birren, B., Nubbaum.C., Lander, E., Ali, A., Allen, N., Anderson, S., Barna, N., Bastien, V., Bloom, T., Boguslavkiy, L., Boukhgalter, B., Conka, A., Cooke, P., DeArellano, K., Dewar, K., Diaz, J.S., Dodge, S., Faro, S., Ferreira, P., FitzGerald, M., Gage, D., Galagan, J., Gardyna, S., Gord, S., Grand-pleirre, N., Hagos, B., Horton, L., Hulme, W., Iliev, I., Johnson, R., Jones, C., Kamat, A., Kols, Kells, C., Landers, T., Levine, R., Lindblad-Toh, K., Liu, G., MacCanthy, M., Meldrim, J., Meneus, L., Mihova, T., Menga, V., McCarthy, M., Meldrim, J., Meneus, L., Mihova, T., Menga, V., Murphy, T., Naylor, J., Nguyen, C., Nicol, R., Norbu, C., Norman, C.H., O'Connor, T., O'Donnell, P., O'Neil, D., O'Ilver, J., Peterson, K., Phunkhang, P., Pierre, N., Raymond, C., Retta, R., Rise, C., Rogov, P., Smith, C., Spencer, B., Stange-Thomann, N., Stojanovic, N., Talamas, J., Tesfaye, S., Theodore, J., Topham, K., Travers, M., Vassillev, H., Viel, R., Vo, A., Wilson, B., Wu, X., Wyman, D., Young, G., Zainoun, J., Direct Submission
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Submitted (06-AUG-2002) Whitehead Institute/MIT Center for Genome Research, 320 Charles Street, Cambridge, MA 02141, USA On Aug 6, 2002 this sequence version replaced gi:20531967.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                All repeats were identified using RepeatMasker:
Smit, A.F.A. & Green, P. (1996-1997)
http://ftp.genome.washington.edu/RM/RepeatMasker.html
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Direct Submission
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Homo sapiens chromosome 18, clone CTD-2146H24 Unpublished
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                                                   Chemistry: Dye-terminator Big Dye; 100% of reads Assembly program: Phrap; version 0.960731 Consensus quality: 132654 bases at least Q40 Consensus quality: 132863 bases at least Q30 Consensus quality: 133865 bases at least Q20 Insert size: 133000; agarose-fp
                                                                                                                                                                                                                         Center project name: L26769
Center clone name: 2146_H_26
----- Summary Statistics
Sequencing vector: Plasmid; n/a;
                                                                                                                                                                                                                                                                                                                                                               Contact: sequence_submissions@genome.wi.mit.edu
                                                                                                                                                                                                                                                                                                                                                                                               Web site: http://www-seq.wi.mit.edu
                                                                                                                                                                                                                                                                                                                                                                                                                                                  Center: Whitehead Institute/ MIT Center
Insert size: 133577; sum-of-contigs
Quality coverage: 17.1 in Q20 bases;
                                                                                                                                                                                                                                                                                                                                                                                                                        Center code: WIBR
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BASE COUNT
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Best Local :
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      171
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        y Match 3.9%;
Local Similarity 44.1%;
                                                                                                                GAAGATTTTCTTACCAATTAAAATTTCGAATTCATATCTCTTGATTATTAAATTAAATTAC 526
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ATATAATCTGTATATATATATATATATCTGTATATAT-ATATATATATATCTCTGTATATATAT
                                                                                                                                                                                                                                                     TGTTATATGTATATGAGTAAATCAAAAAAGAGTATTGAATTGAAGTGTAAACATATTTCGTT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            GAGTGTGAATATCCGTTTATCGATCACTCCAATCATGATTATGATTCTTGTGCTAATCCA 586
                                                                                                                                                                   TTGGTTCTGGATTAGGTTTATTTGATCATAATTACATGCA-TCATTTCTTTGATTACTAT
                                                                                                                                                                                                                                                                                            ATAAAGGAAATAATCGATTCCATTTGGTTGGATTACACAGTTAAGTTTTTGTGTTTTCTTT 290
                                                                               NOTE: This is a 'working draft' sequence. It currently consists of 4 contigs. Gaps between the contigs are represented as runs of N. The order of the pieces is believed to be correct as given, however the sizes of the gaps between them are based on estimates that have provided by the submittor. This sequence will be replaced
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            the accession number will be preserved.

1 716: contig of 716 bp in length
717 816: gap of 100 bp
817 1487: contig of 671 bp in length
1887: gap of 100 bp
1588 1993: contig of 406 bp in length
1994 2093: gap of 100 bp
2094 133877: contig of 131784 bp in length.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        by the finished sequence as soon as it is available
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Quality coverage: 17.0 in Q20 bases; sum-of-contigs
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Conservative
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2094. .133877
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24268 c 24460 g 43475 t
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817. .1487
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 /organism="Homo sapiens"
/db_xref="taxon:9606"
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/clone_lib="CITD1 Human BAC"
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Pred. No. 1.5e-09;
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                                        GATATTCGTTAAAATTTGCGATAACGATTGTGAAAAATATTTTATTTGTTAGCTGATCTC
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                                                                         AGAAAACGATTTTTCTTGGATTCCATTCAATGATCTAAAATGCATAGATCTTTTGGGTTA 1486
                                                                                                                                                                                                                                                TACGATCACTGCAAATATCATTCTTGGTTGGTCAACAATAAAAAACAAAAAACAAGAAAAAA 1426
                                                                                                                                                                                                                                                                                                AGTTATGTGATGTCGATAAATGAAATTCACACGCGTGGTAATAATTATGGGACCGTATGT 1366
                                                                                                                                                                                                                                                                                                                          TATTATATATATATATATATATATATA - TTTTCATATATATTATTATATATATATATATATAT
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           TGTTTCGTTTCTCTTAACTATATTATCGCGGATATATGATAACAATGATATATCACAA 946
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                                                                                               TGCATCTTTAACATATTTATTGTTAGTTGGAATTTAATAAGAGCGAACTTGTAACATTAC
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        TAACAGATAGAAAACTATTTTGTTGTGGAATGGAAGTAGTAATATACATTAAGCAAATTT 2266
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   TATTTTCGCGATGCATGAAGGATAAACCTAATGACTTTAATTTTTTGAAAATGTAACCCT 1786
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ATTATATAAATAATTATTAAATATTATATTTTTATAT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  AACAATATTATAAAATATGATGCCTATAATGTATTTCCTATGTTCTTAAAATATTTTTT 2026
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 AACAGCTGAGTATTACATTTTAAATTTAAAGACAAAATTTTTGAAAAATGTTATAATTTCT 1966
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         TTTACTCATAGATTAATTACCGTATGTTTTTGTTGCCATAATGACAGCCTCTACAACTGT 1846
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ATTAATATTTTTTGAAATCTACAAATTATTAATATTTAGTCAATAACAATGCATAGAAAG 2146
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Plasmodium falciparum MAL3P5, complete sequence.
AL034556 AL008971 AL008972 AL008978 AL010141 AL010153
AL010206 AL010210 AL139179
AL034556.3 GI:7711064
HTG; centromaca:
  Bowman, S., Lawson, D., Basham, D., Brown, D., Chillingworth, T., Churcher, C.M., Craig, A., Davies, R.M., Devlin, K., Feltwell, T., Gentles, S., Gwilliam, R., Hamlin, N., Harris, D., Holroyd, S., Hornsby, T., Horrocks, P., Jagels, K., Jassal, B., Kyes, S., McLean, J., Moule, S., Mungall, K., Murphy, L., Oliver, K., Quail, M.A., Rutter, S., Skelton, J., Squares, R., Squares, S., Sulston, J.E., Whitehead, S., Woodward, J.R., Newbold, C. and Barrell, B.G.
                                                                                                                                                                                                                                                  HTG; centromere; CTRP protein; initiation factor E4; Serine/threonine protein phosphatase. Serine/threonine protein phosphatase. Plasmodium falciparum 3D7. Plasmodium falciparum 3D7 plasmodium falciparum falciparum 3D7 plasmodium falciparum falcipar
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For more information about this sequence or the Malaria Project, see http://www.sanger.ac.uk/Projects/P_falciparum.

Location/Oualiffere
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99376085
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On or before May 14,
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Direct Submission
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      The
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               falciparum
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                                                                             complement(3354..6644)
/gene="PPC0580c, MAL3P5.2"
complement(3354..6644)
/gene="PPC0580c, MAL3P5.2"
/note="PPC0580c (MAL3P5.2), Hypothetical protein,
1097 aa, possible signal sequence, predicted using
hexExon"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         RSPQIYKKFKKSKIKNVSFKKKQKFPLFLFENLKKGFSFLGFWRNQYDQKYIDDVIS
AINNLTRIKQVTHKKKSNEFTKENIKQTLLHCVFSKIDFKINLLSYIIKHFQMSNIT
VHSILNQISEKYVEKKDAENYLAHLFILKDENITLESWAMH MDFFKSKQKVIECIRG
IKSKKKKKNLSIYINLFICTLIYFTYCMCLLIKYISHLCIFFFFFFFFECYNILER
IYEECVGDLIRKKIERYNLYCEKKKIKFHMKDAIKKMEINMKDDLYENYHVDELLRC
FTMKLNIERNNKNIIRSNUTOLISIDKDWYMNNPIDVNINNISLDEK IKEQFENP
DDENLKELKDTYGQFQLENDNIIKYIEEDQPLYNINDSNINDNNNINTMKNKHKIK
DTYNDDDDYDVEKEEDDLYIGKHIDDYIYKNTIGMKSLEEFKNQFIBQADIEPONFLS
NVNLDQHGRVKSNDENTKSTEHIKNKNTINKGYDTELLGXIEYLFKFYQYDIINISND
ISNNEINJIKLKKKLNQSDEDINLTSDLIYERLAFTXVLMYJQKIEYLFKFYQYDIINISND
TSNNEINJIKLKKKLNQSDEDINLTSDLIYERLAFTXVLMYJQKIEYLFKFYQYDDINISND
TSNNEINJIKKKKTUNGSDEDINLTSDLIYERLAFTXVLMYJQKIEYLFKFYQYDDINISND
TSNNEINJIKKKKTUNGSTEINKNKTINKGYDTELLOMENDRIKKNNQMENQKNSKNY
PIIKKBKTVLDLLNYGYKIVMSPDVDNSLFEKTKIDSIPNEKDKNNQMENQKNSKNY
                                                                                                                                                                                                                                                     PFC0575w (revised)"
complement();
                                                                                                                                                                                                                                                                                                      1024. .1029
/gene="PFC0575w,
/note="predicted
                                                                                                                                                                                                                                                                                                                                                                                            /gene="PFC0575w, MAL3P5.1"
/note="predicted splice acceptor
(revised of PFC0575w)"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            /product="Hypothetical
/protein_id="CAB38969.;
/db_xref="GI:7711065"
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/product="Hypothetical
/protein_id="CAB38968.1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 /gene="PFC0575w,
/note="predicted
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        join(322. .603,826. .1023,1197.
/gene="pfC0575w, MAL3P5.1"
join(322. .603,826. .1023,1197.
                                                      /codon_start-1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 /gene="PFC0575w, MAL3P5.1"
/note="PFC0575w (MAL3P5.1), Hypothetical protein, len:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        translation-"MYLKNVYIYISSCFILFDLCFSFHLLKMKYKNHMNNMKSVTFFL/
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        /db_xref="SPTREMBL:097258"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               /strain="3D7"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         /organism="Plasmodium
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        chromosome=
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  /db_xref-"taxon:36329"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      .86827
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   MAL3P5.1"
1 splice donor :
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Barrell, B.
                                                                                                                                                                                                                                                                                                                                         MAL3P5.1"
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  u protein,
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                                                                                                                                                                                                                                                                                                               donor
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                            PFC0580c
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             /translation="MKKKKHYFSIKFVNVDKNKYYLCSKDYIRIINYMIGLHIFRLL
QKIPHIYFANEQIASSFFESHKNYRVTKEDIIDGIEKCWFNITDYLISESIKQDNDFS
NDIKTTVTAHKNKHDQLLTTSYSNKKIDTVNASFQWAQSPEYIFLNIKFSHRWSSPGA
LKVKDEEIVSKKNNFSFSALSNDSNSVTKKYIVDLTLLDNIIESETKYNFASVGKVYV
                       'gene="PFC0581w"
                                                                                                                                             'gene="PFC0581w"
                                                                                                                                                                                                                                         PFC0581w
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    QNFLKEEKNNSDKLQDDIDEDEEKYFDEEILREAKKKSEEYDKDDEEL"
                                                                              'gene="PFC0581w"
                                                                                                                                                                                                          /gene="PFC0581w"
                                                                                                                                                                                                                                                    'note="potential
                                                                                                                                                                                                                                                                        /gene="PFC0581w"
                                                                                                                                                                                                                                                                                                                 note="potential"
                                                                                                                                                                                                                                                                                                                                   /gene="PFC0581w"
                                                                                                                                                                                                                                                                                                                                                                                             7830. .7835
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                /product="hypothetical protein,
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   FYDHINSSSNRCSFKNLKKQQTDDNTKHIIMGKEKYPMNKSDHEKKNNNTCGNINIEK
DOKKOILKKIYFLKGNKLDDIQILNELYVMIYMRLLFECSLKLISIKKNIHLLEKKME
FDKDNKIIYLNSADYMNNLRHNILKRESKNEERENINSFASFPFLLSKNIIYFEDEIG
RSRDNTIYNNYDKETNKTTTNNNNNDNNDNICSNNDHICSNNNDHICSNNNDHICSN
                                                                                                                                                                                                                                                                                                                                                                           'note-"potential
                                                                                                                                                                                                                                                                                                                                                                                                                                                           /gene="PFC0581w"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    tentative"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             8302. .8368,8568. .8641,
9369. .9505,9613. .9838)
/gene="PFC0581w"
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KNTNISSYSTYNNMEKENINIYDKYNIHNFYTEKSISYKDENCQHITLNMIYLLNQTY
DNICRICLNTNTNIYINFYMINILKYICYKNYEIILLNYNHIEDMKKKINQKNNTNTS
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/db_xref="G1:4493932"
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/translation="MLGEKRRNVEYLLVSVPSLFAYFLKRHKDNENNYETLINNNDIE
KIKKIRIHNKCSYIPLLFLNIYDSYIYKNKILRWLYEKFRKRRDKEEYYYINMYRK
KRREAIKYNFISDEONLFNKFYIYEIYVLEYSLKYGILSPHLSLYILKNISEHCYNIYP
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AC105425.2 GI:18151067
AC105425.2 PHASE1; HTGS_DRAFT;
                                                                                                                                                                                                     205130 bp DNA linear E
Homo sapiens chromosome 7 clone RP11-776N17, WORKING
SEQUENCE, 12 unordered pieces.
                        2 (bases 1 to 20)
Waterston, R.H.
Direct Submission
                                                                            The sequence of Homo sapiens clone
                                                                                        1 (bases 1 to 205130)
Waterston, R.H.
                                                                                                                  Eukaryota; Metazoa; Chordata; Mammalia; Eutheria; Primates;
                                                                                                                                              Homo sapiens
                                                              Jnpublished
                                                  to 205130)
                                                                                                                  Craniata; Vertebrata; Euteleostomi; Catarrhini; Hominidae; Homo.
                                                                                                                                                                      HTGS_FULLTOP
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DRAFT
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Submitted (04-JAN-2002) Genome Sequencing Center, Washington University School of Medicine, 4444 Forest Park Parkway, St. MO 63108, USA
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COMMENT
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Consensus quality: 198378 bases at least Q40
Consensus quality: 199230 bases at least Q30
Consensus quality: 200198 bases at least Q20
Topoct 6:00.000000.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Center: Washington University Genome Center code: WUGSC
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Quality coverage: 10.60 in Q20 bases; agarose-fp Quality coverage: 10.87 in Q20 bases; sum-of-contigs
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Center project name: H_NH0776N17
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Contact: submissions@watson.wustl.edu
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Web site:http://genome.wustl.edu/gsc/index.shtml
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Sequencing
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           runs of N, but the exact sizes of the gaps are unknown. This record will be updated with the finished sequence as soon as it is available and the accession number wil be preserved.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 NOTE: This is a 'working draft' sequence. It currently consists of 12 contigs. The true order of the pieces is not known and their order in this sequence record is
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                arbitrary. Gaps between the contigs are represented as
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                               vector_side:left"
                                                    clone_end:T7
                                                                                        /note="assembly_name:Contig109"
4737. .25187
                                                                                                                                                                                                                                    /organism="Homo sapiens"
/db_xref="taxon:9606"
/chromosome="7"
                                                                                                                                                                                                                                                                                                           Location/
                                                                     note="assembly_name:Contig110"
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Matches 998; Conserv
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                                                                                                                                                                                                                                                                      TTATCAAAGAGAATAAGAGATGACAACCAAAAGGTTGTGGAATAATGGTCCCTGCCAGCT 727
                                                                                                                                                                                                                                                                                                                                         TGAGAAAAAACCGAAAATAAGAAAAGGGAAAGAGTAGTGACCCATGGAGTATGTGAATAA 667
                                                                                                                                                                                                                                                                                                                                                                               TTTCTATAATATACATATTGTATATTATATTATATATAGTATA----TACATATTGTAT
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204024. .205130
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82414. .122098
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200454. .201279
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Pred. No. 2.5e-09;
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TGCAAATATTAAATTAGGAATTCAATGCTACTATCAATAGAAGAAACAGCTGAGTATTAC
                                                                                                                                                                                                                                                  TTACCGTATGTTTTGTTGCCATAATGACAGCCTCTACAACTGTGATAGTCAATTTTTTC 1862
                                                                                                                                                                                                                                                                                         GAAGGATAAACCTAATGACTTTAATTTTTTGAAAATGTAACCCTTTTACTCATAGATTAA 1802
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                                                                                                                          ACTAGTATGTGATTATTCCAAATACATACTTTGGATGTTTAAACTTAATCTTGTTTCTTC 1682
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                                                                                                                                                                                                                                                         Submitted (28-JUN-1994) Laurie S. Kaguni Ph.D, Dept. of Biochemistry, Michigan State University, East Lansing,
                                                                                                                                                                                                                                                                                                                                                                                                                                     Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota; Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha; Ephydroidea; Drosophilidae; Drosophila.
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Mitochondrion Drosophila melanogaster
Eukaryota; Metazoa; Arthropoda; Hexapoda; Inse
Neoptera; Endopterygota; Diptera; Brachycera;
Ephydroidea; Drosophilidae; Drosophila.

1 (bases 12511 to 12682)
    Drosophila
                                                                                                                Clary, D.O., Wahleithner, J.A. and Wolstenholme, D.R. Transfer RNA genes in Drosophila mitochondrial DNA:
                                                                                                                                                                                      Drosophila mitochondrial DNA: a novel gene order Nucleic Acids Res. 10 (21), 6619-6637 (1982)
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                                                                        Nucleic
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Bruljn, M.H.
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Lewis, D.L., Farr, C.L., Farquhar, A.L. and i Sequence, organization, and evolution of 1 Drosophila melanogaster mitochondrial DNA Mol. Biol. Evol. 11 (3), 523-538 (1994)
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88174373
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Lewis, D.L., Farr, C.L. and Raguni, L.S.
Drosophila melanogaster mitochondrial DNA: complucieotide sequence and evolutionary comparisons
Insect Mol. Biol. 4 (4), 263-278 (1995)
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96423163
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Science 258 (5086),
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Ballard, J.W., Olsen, G.J.,
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                                                                                                                complement(97. .165)
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171. .239
                                                                                                                                                                                                                                                                                                   State University,
           /product="NADH dehydrogenase
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                                                                                                                                                                                 /note="derived from new and previously submitted
sequences; sequence is a composite containing sequences
obtained from different Drosophila melanogaster strains
                                                                                                                                                                                                      sequences;
                                                                                                                                                                                                                                           /organism="Drosophila melanogaster"
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                                                                                                                                                          /product="tRNA-Ile"
                                                                     codon_start=1
                                                                                                                                                                                                                              /db_xref="taxon:7227"
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/product="cytochrome c oxidase subunit I"
protein_id="Aac47812.2"
/protein_id="Aac47812.2"
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LLPPALSLLLVSSMVENGAGTGWTVYPPLSAGIAHGGASVDLAIFSLHAGINSNINTSF
UNFITTVINKRSTGISLDRMPLFVWSVVITALLLLLSLPVLAGAITMLLTDRNLNTSF
EDPAGGGDPILYQHLFWFFGHPEVYILILPGFGMISHIISQESGKKETFGSLGMIYAM
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LKSGAAPFHFWFPNMEGLTWMAALMSTWOK 1 APLIL 1SYLNIKYLLLISVIE
GAIGGLNOTSLEKKLMAFSINHLGMLMLSSLMISESIMLLIFFFYSELSFYLTFHENEI
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IHWYPLFTGLTLNNKWLKSHFIIMFIGVNLTFFPQHFLGLAGMPRRYSDYPDAYTTWN
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3907. .4068
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join(1470. .1472,1474. .3009)
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                                                                                                                                                                                                                                                                                                                                                                                           /protein_id="AAC47814.1"
/db_xref="GI:1166533"
                                                                                                                                                                                                                                                                                                                                                                                                                                     /product="ATPase 8"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                /transl_table=5
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                                             codon_start=1
                                                                                                                                                                                                                                                                                                   /codon_start=1
                                                                                                                                                                                                                                                                                                                                                                   translation="MPQMAPISWLLLFIIFSITFILFCSINYYSYMPNSPKSNELKNI"
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                                                                  TTTTTAAAAAATAAACAAAAATTTTTAATAAATAAATTTTTATAATGAAATATAATTTAT 17656
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                                                                                                             ATTGAGAAAAAACCGAAAATAAGAAAAAGGGAAAGAGTAGTGACCCATGGAGTATGTGAAT 665
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5608. .5961
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VLGNIITILTVYQWWRDVSREGTYQGLHTYAVTIGLRWGMILFILSEVLFFVSFFWAF
FHSSLSPAIELGASWPPMGIISFNPFOIPLLWTAILLASGVTVTWAHHSLMENNHSQT
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6184. .6251
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6055. .6118
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/protein_id="AAC47817.1"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    CLLRHLNNHFSKNHHFGFEAAAWYWHFVDVVWLFLYITIYWWGG"
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/db_xref="GI:1166535"
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GAAAACGATTTTTCTTGGATTCCATTCAATGATCTAAAATGCATAGATCTTTTGGGTTAC 1487
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                                                                     GATAGTCAATTTTTTCTGCAAATATTAAATTAGGAATTCAATGCTACTATCAATAGAAGA 1906
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ATGCATGGTGCGATTCAGAATTGGGACAACAATGAAAACGGAATTAAAATATTAACTTTA
                                              TAACAGATAGAAAACTATTTTGTTGTGGAATGGAAGTAGTAATATACATTAAGCAAATTT
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## ALIGNMENTS

DWF4; cytochrome P450 enzyme; brassinosteroid; 22alpha-hydroxylation; plant phenotype; cell elongation; ss. /\*tag= e 3504..3828 /\*tag= f /\*tag= d 3424..3503 /\*tag= a 3060..3125 /\*tag= b 3203..6110 /\*tag= c /\*tag= c /product= "DWF4" /note= "contains introns" Location/Qualifiers 203..3423 ,=3913

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AAL15210/c
ID AAL15210 standard; cDNA; 883 BP.
XX
AC AAL15210;
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DT 07-DEC-2001 (first entry)
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AX
BE Human breast cancer expressed polynucleotide
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KW Human; breast cancer; cell marker; cytostatic
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                                                                                                                                                                                                                                                                                                                                                                                                                  The invention relates to human breast cancer expressed polynucleotides (AAL07544-AAL26789) and methods of assessing whether a patient is afflicted with breast cancer by examining the correlation between the expression of certain markers and the cancerous state of breast cells.
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                                                                                                                                                                                                                                                                                                                                                                       polypeptides are also useful for isolating compounds with activity.
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                   TAGTCAATTTTTTCTGCAAATATTAAATTAGGAATTCAATGCTACTATCAATAGAAGAAA 1908
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                                                                                               TTTTCGCGATGCATGAAGGATAAACCTAATGACTTTAATTTTTTGAAAATGTAACCCCTTT 1788
                                                                                                                                   AATCTTGTTTCTTCCTACGGTATAAATATTAATCATCGAGGTAAAAAAAGTTTTGTCTTA 1728
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2000US-0211315.
2000US-0220534.
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Sequence number

Listing; German human

Claim 1;

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RESULT 3
ABL32427
Nucleic acid comprising fragment of chemically modified gene, useful for diagnosis and treatment of diseases associated with abnormal
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           antiarteriosclerotic; antianaemic; cytostatic; nootropic; neuroprotective; anti-HIV; anticonvulsant; ophthalmological; antirheumatic; antiarthritic; antidiabetic; antipsoriatic; antiarthritic; antidiabetic; antipsoriatic; antiinflammatory; cancer; eye disease; arteriosclerosis; anaemia; acute myeloid leukaemia; Alzheimer's disease; AIDS; epilepsy; neurofibromatosis; rheumatoid arthritis; psoriasis; bowel disease
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Matches 407
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                                     AACGGAATTAAAATATTAACTTTAAAATAAATAAAAATTTGAGTAAATGTGTTTTCTGAC
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                                             The invention relates to a nucleic acid, which comprises a segment of the chemically pretreated DNA of genes associated with DNA transcription from one of 346 sequences, and an oligomer, in particular an oligonucleotide one of 346 sequences, and an oligomer, in particular an oligonucleotide or peptide nucleic acid (PNA)-oligomer that hybridises to or is identical to the chemically pretreated DNA of genes associated with DNA conscription. The set of oligomer probes are useful for detecting the cytosine methylation state and/or single nucleotide polymorphisms (SNPs) in a chemically pretreated genomic DNA. The nucleic acids are useful for diagnosing or treating diseases associated with DNA transcription (particularly with the methylation status), e.g. adenosine deaminase deficiency, viral infection, retroviral infection, Sezary syndrome, tuberculosis, developmental disorders, psoriasis, Reger's syndrome, cubroculosis, developmental disorders, psoriasis, Reger's syndrome, neurological disorders, neurodegenerative disorders, Warardenburg syndrome, Niemann-Pick disease, myelodysplastic syndrome, myocardial confarction, hypertension, anglogenesis, erythropoiesis, congenital heart conscripted genomic DNA molecules of the invention
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30-JUN-2000;
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The present invention provides a number of human immune system associated genes which are modified by the methylation of cytosines. The sequences can be used in the diagnosis and treatment of immune system disorders, including eye diseases such as retinopathy, neovascular glaucoma and macular degeneration, arteriosclerosis, anaemia, cancer, acute myeloid leukaemia, Alzheimer's disease, AIDS, epilepsy, neurofibromatosis, rheumatoid arthritis, psoriasis and inflammatory/ulcerative bowel
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Nucleic acid comprising for diagnosis and treatm cytosine methylation -
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TAGGAATTCAATGCTACTAATAGAAGAAACAGCTGAGTATTACATTTTAATTTAAAG 1936
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                                                                                                                                                            TTTAATTTTTGAAAATGTAACCCTTTTACTCATAGATTA----ATTACCGTATGTTTTT
                                                                                                                                                                                                                                                                   TAGATTTATTAAAGATTTTTTTATTGTTTGTAAAATAATTTGTAAGTTTTTGATTTTGGAAT
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Pred. No. 0.00029;
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WPI; 2002-130909/17
                                                                                                                                                                                                                                                                                                                                                                                                                                         Human; immune system disease; cytosine methylation; antiasthmatic; antiarteriosclerotic; antianaemic; cytostatic; nootropic; neuroprotective; anti-HIV; anticonvulsant; ophthalmological; antirheumatic; antiarthrito; antidiabetic; antipsoriatic; antinflammatory; cancer; eye disease; arteriosclerosis; anaemia; acute myeloid leukaemia; Alzheimer's disease; AIDS; epilepsy; neurofibromatosis; rheumatoid arthritis; psoriasis; bowel disease;
                                                                                                                                                    30-JUN-2000;
01-SEP-2000;
                                                                                                                                                                                                                            02-JUL-2001; 2001WO-EP07537
                                                                                                    (EPIG-)
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                                                                                               EPIGENOMICS AG
                                            Piepenbrock C,
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Best Local Similarity
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  genes which are modified by the methylation of cytosines. The sequence can be used in the diagnosis and treatment of immune system disorders, including eye diseases such as retinopathy, neovascular glaucoma and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     macular degeneration, arteriosclerosis, anaemia, cancer, acute mye leukaemia, Alzheimer's disease, AIDS, epilepsy, neurofibromatosis, rheumatoid arthritis, psoriasis and inflammatory/ulcerative bowel diseases. The present sequence is a gene of the invention.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       The present
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Nucleic acid comprising fragment of chemically modified gene, useful for diagnosis and treatment of diseases associated with abnormal cytosine methylation
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Claim 1; SEQ ID NO 399;
      AATGCATGGTGCGATTCAGAATTGGGACAACAATGAAAACGGAATTAAAATATTAACTTT
                                                        ATATAATATATGTTTATATATATAATATATGTAAATATATATATATGTAAATATATATGTA
                                                                                                                                                         ATTAATATTTTTTGAAATCTACAAATTATTAATATTTAGTCAATAACAATGCATAGAAAG
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              invention provides a number of human immune system associated are modified by the methylation of cytosines. The sequences
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Pred. No. 0
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06-APR-2000;
07-APR-2000;
30-JUN-2000;
01-SEP-2000;
                                                                                                                                                    Sequences AAS45296-AAS45520 represent chemically pretreated genomic DNA molecules associated with the cell cycle and specific PCR primers of the invention. The sequences are useful for detecting the methylation state of all CpG dinucleotides in a sequence and therefore for analysing associated diseases. By analysing cytosine methylations in the pretreated DNA, genetic and/or epigenetic parameters for the diagnosis and therapy of existing diseases or the predisposition to specific diseases can be ascertained. The parameters may be compared to another set of genetic and/or epigenetic parameters, the differences serving as basis for diagnosis and/or prognosis events which are disadvantageous to patients. The sequences of the invention are useful for the diagnosis and therapy of HIV infection, neurodegenerative disorders, graft-versus-host disease,
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                                                                                                                                                                                                                                                                                                                                                            cytosine methylation state e.g. arthritis, cancer, aging, arteriosclerosis comprising fragments of chemically modified essectated with cell cycle -
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Cell cycle; human; CpG dinucleotide; cytosine methylation; HIV; aging; human immunodeficiency virus; neurodegenerative disorder; solid tumour; graft-versus-host disease; glomerular disease; Lewy body disease; cancer; arthritis; arteriosclerosis; anti-HIV; neuroprotective; antiarthritic;
                                                                                                  Sequence
                                                                                                                                                                                                                                                                                                                                             Claim 1;
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                                                                                                  15732
                                                                                                                                                                                                                                                                                                                                            SEQ ID No 93; 28pp;
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2000DE-1019173.
2000DE-1032529.
2000DE-1043826.
                                             Conservative
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                                                                                                  B₽;
                                                                                                                              solid
                                                                                                                                          disease, Lewy body disease,
                                                                                                 4638 A;
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                                                                                                 70 C;
                                          0,
                                          Score 82.6; DB 2
Pred. No. 0.00032
0; Mismatches 57
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RESULT 8 ABK28233/c

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CCCTATCTTTTCA 5802
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                                            ATTTTTCAAACATAATTAACAAACTTACTTAAAAAACTTTATCTTACTTAAATAAAATTT
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23-APR-2002

(first entry)

ABK28233 standard;

DNA;

15732

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The invention relates to a nucleic acid, which comprises a segment of the CC chemically pretreated DNA of genes associated with DNA transcription from CC one of 346 sequences, and an oligomer, in particular an oligonucleotide CC or peptide nucleic acid (PNA)-oligomer that hybridises to or is identical CC transcription. The set of oligomer probes are useful for detecting the CC transcription. The set of oligomer probes are useful for detecting the CC in a chemically pretreated DNA of genes associated with DNA cC diagnosing or treating diseases associated with DNA transcription CC (particularly with the methylation status), e.g. adenosine deaminase CC diagnosing or treating diseases associated with DNA transcription CC (particularly with the methylation status), e.g. adenosine deaminase CC haematological disorders, immunological disorders, yspharome, e.g. achenosine deaminase CC tuberculosis, developmental disorders, psoriasis, Rieger's syndrome, CC syndrome, Nuemann-pick disease, myelodysplastic syndrome, myocardial cc infarction, hypertension, angiogenerative disorders, waardenburg CC syndrome, arthritis, polyglutamine disorders, solid tumours associated genomic DNA molecules of the invention.

CC specification but was obtained in electronic format directly from the CC European Patent Office.
                          Query Match
Best Local :
         Matches 453;
                                                                             Sequence 15732
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     WPI;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Claim 1; SEQ ID No 107; 32pp;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   New nucleic acids or oligomers, useful for diagnosing or treating diseases associated with DNA transcription, e.g. immunological disorders, Werner syndrome, psoriasis, myocardial infarction, solid
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30-JUN-2000;
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                        Similarity
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       Conservative
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; 2000DE-1019173.
; 2000DE-1032529.
; 2000DE-1043826.
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   0;
Score 82.6; DB 24;
Pred. No. 0.00032;
0; Mismatches 574;
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06-APR-2000;
07-APR-2000;
30-JUN-2000;
 2050
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                                                                                                                                                                                                        invention. The sequences are useful for detecting the methylation state of all CpG dinucleotides in a sequence and therefore for analysing associated diseases. By analysing cytosine methylations in the pretreated DNA, genetic and/or epigenetic parameters for the diagnosis and therapy of existing diseases or the predisposition to specific diseases can be ascertained. The parameters may be compared to another set of genetic and/or epigenetic parameters, the differences serving as basis for diagnosis and/or prognosis events which are disadvantageous to patients. The sequences of the invention are useful for the diagnosis and therapy of HIV infection, neurodegenerative disorders, graft-versus-host disease, aging, glomerular disease, Lewy body disease, arthritis,
                         1884 TCAATGCTACTATCAATAGAAGAAACAGCTGAGTATTACATTTTAAATTTAAAGACAAAAT
                                                                                                                                                                                                                                                                                                                                                                                                                                                      Designing primers and probes for analysing diseases associated with cytosine methylation state e.g. arthritis, cancer, aging, arteriosclerosts comprising fragments of chemically modified genes
                                                                                                                                                                     Sequence 5689
                                                                                                                                                                                                                                                                                                                                                                   Sequences AAS45296-AAS45520 represent chemically pretreated genomic I molecules associated with the cell cycle and specific PCR primers of
                                                                                                                                                                                                                                                                                                                                                                                                                                           associated with cell cycle
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                                                                                                                                                                                                                                                                                                                                                                                                                 Claim 1;
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Local Similarity
es 285; Conserv
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2000DE-1019173.
2000DE-1032529.
2000DE-1043826.
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                                                                                                              Conservative
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                                                                                                                                                                      BP; 1490 A;
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                                                                                                                          Score 81.6;
Pred. No. 0.
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Fragments genes and

of chemically modified genes associated with tumour suppressor oncogenes, useful in designing primers and probes for diseases associated with cytosine methylation state e.g.

2001-602752/68

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ID AAS46426 standard; DNA; 5689
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06-APR-2000;
07-APR-2000;
30-JUN-2000;
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cancer; tumour; CpG dinucleotide; single-nucleotide polymorphism;
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                                                                                                                                                                                                                                                                                                                                                                                                                                              ТАТААТСТАТСААААЛТАААТАААТТААТТААЛТААТТААСТААТАТТААТААЛАААА 1571
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      TTTTGAAAAATGTTATAATTTCTAACAATATTATTAAAATATGATGCCTATAATGTATTT
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                                                                                                EPIGENOMICS
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; 2000DE-1019058.
; 2000DE-1019173.
; 2000DE-1032529.
; 2000DE-1043826.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             CC The invention relates to a nucleic acid comprising a sequence of 18 CC bases, of a segment of chemically pretreated DNA (CP DNA) e.g. with CC bisulphite, of genes associated with tumour suppression and CC oncogenes having a sequence taken from 536 (actually 533 since CC oncogenes having a sequence taken from 536 (actually 533 since CC complementary to (cs). The nucleic acid may be a CC peptide nucleic acid-oligomer (PNA) of at least 9 nucleotides and may CC form part of a set of probes for detecting the cytosine methylation state and/or single nucleotide polymorphisms and also to be used in an CC array for analysing diseases associated with CpG dinucleotides e.g. CC ascertaining genetic and/or epigenetic parameters for the diagnosis cancers and tumours. The probes can also be used in a method for CC ascertaining genetic and/or epigenetic parameters for the diagnosis CC diseases, by analysing cytosine methylations. The parameters may be CC and/or therapy of existing diseases or the predisposition to specific CC diseases, by analysing cytosine methylations. The parameters may be CC differences serving as basis for diagnosis and/or epigenetic parameters, the CC differences serving as basis for diagnosis and/or prognosis events which CC complementary sequences derived from tumour suppressor genes and CC complementary sequence with even numbered Seq ID numbers are the CC complementary sequence of the corresponding odd numbered sequence (e.g. ID 2 and IDI, ID 536 and ID 535, except for those whose partner sequence CC is missing).
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Best Local
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       1824 ATAATGACAGCCTCTACAACTGTGATAGTCAATTTTTTCTGCAAATATTAAATTAGGAAT 1883
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Sequence 5689 BP; 1490 A; 207 C; 1277 G; 2707 T; 8 other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ftp.wipo.int/pub/published_pct_sequences
AAAACGGAATTAAAATATTAACTTTAAAATAAATAAAAAT
                                                                       TGTTATCTAGTAGGTGTAATTA-ATGCATGGTGCGATTCAGAATTGGGACAACAATG
                                                                                                                  GTAGTAATATACATTAAGCAAATTTTAAAAAATTATATAAGCCTATACGCGCTCAAAGTA
                                                                                                                                                                                        TAGTCAATAACAATGCAT-AGAAAGTTCCCAAAAAATTTTTGTTAACAGAAACTTCCAAA
                                               TTTTTTTTTTTATGGAACAAAAATAACAGATAGAAAACTATTTTGTTGTGGGAATGGAA
                                                                                                                                                                                                                                                                                                                                    AGTTGGT-GAATTCAAATATCTCCATTAATATTTTTTGAAATCTACAAATTATTATTATTATATATT
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                                                                                                                                                                                                                                                              285;
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Pred. No. 0.00044;
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RESULT 11
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pNA; cytosine methylation state; SNF; retroviral infection; gene; ds; single nucleotide polymorphism; adenosine deaminase deficiency; cancer; viral infection; Sezary syndrome; haematological disorder; tuberculosis; immunological disorder; werner syndrome; developmental disorder; psorlasis; Rieger's syndrome; neurological disorder; erythropolesis; neurodegenerative disorder; waardenburg syndrome; niemann-pick disease; myelodysplastic syndrome; myocardial infarction; hypertension; arthritis; angiogenesis; congenital heart disease; HDR syndrome; gene therapy; polyglutamine disorder; solid tumour. PNA-oligomer;

06-APR-2000; 2000DE-1019058 07-APR-2000; 2000DE-1019173 30-JUN-2000; 2000DE-1032529 01-SEP-2000; 2000DE-1043826 WPI; 2002-090046/12 Olek A, 06-DEC-2001. (EPIG-) 06-APR-2001; 2001WO-EP03973 W0200192565-A2 Unidentified. EPIGENOMICS AG Piepenbrock C,

New nucleic acids or oligomers, useful for diagnosing or treating diseases associated with DNA transcription, e.g. immunological disorders, Werner syndrome, psoriasis, myocardial infarction, solid tumours or cancer

Claim 1; SEQ ID No 100; 32pp; English

CC chemically pretreated DNA of genes associated with DNA transcription from CC one of 346 Sequences, and an oligomer, in particular an oligonucleotide or peptide nucleic acid (PNA)-oligomer that hybridises to or is identical transcription. The set of ollgomer probes are useful for detecting the cytosine methylation state and/or single nucleotide polymorphisms (SNPs) and chemically pretreated genomic DNA. The nucleic acids are useful for detecting the cytosine methylation state and/or single nucleotide polymorphisms (SNPs) and chemically pretreated genomic DNA. The nucleic acids are useful for disposing or treating diseases associated with DNA transcription comparticularly with the methylation status), e.g. ademosine deaminase deficiency, viral infection, retroviral infection, Sezary Syndrome, actuberculosis developmental disorders, psoriasis, Rieger's syndrome, comparative disorders, werner syndrome, comparative disorders, manufaction, hypertension, angiogenerative disorders, Warardenburg comparative, angiogenesis, erythropoitesis, congenital heart correct sequences ABK28127-ABK28472 represent DNA transcription consociated genomic DNA molecules of the invention.

Note: The sequence data for this patent did not form part of the printed corrobers patent office. European Patent Office

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RESULT 12
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Best Local Similarity
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02-JUL-2001; 2001WO-EP07537.
                       03-JAN-2002.
                                                                                                     acute myeloid leukaemia; Alzheimer's disease; AIDS; neurofibromatosis; rheumatoid arthritis; psoriasis;
                                                                                                                           neuroprotective; anti-HIV; anticonvulsant; ophthalmological;
antirheumatic; antiarthritic; antidiabetic; antipsoriatic;
antiinflammatory; cancer; eye disease; arteriosclerosis; anaemia;
                                                                                                                                                                antiarteriosclerotic;
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                                             WO200200928-A2
                                                                                                                                                                            Human;
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                                                                                                                                                              immune system disease; cytosine methylation; antiasthmatic;
teriosclerotic; antianaemic; cytostatic; nootropic;
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Pred. No. 0.
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01-SEP-2000;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Claim 1; SEQ ID NO 1027;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  (EPIG-)
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hes 410;
TTTTTTTAGAAAGATTTTTTATAGTTTGGGGGTAGAATTTAGTGTAATATTTATATTGTTT
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  GTATTTCCTATGTTCTTAAAATATTTTTTTTTATATTTAGTTATAAATACATTATGAACC
                                                                                                                                              CAAAATTTTTGAAAAATGTTATAATTTCTAACAATATTATTAAAATATGATGCCTATAAT
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                                                                                                                                                                                                                                     TAATCATCGAGGTAAAAAAAGTTTTGTCTTATTTTCGCGATGCATGAAGGATAAACCTAA 1757
                                                                                                                                                                                                                                                                                                                                                                                                                                      TICCAAATACATACTTIGGATGTTTAAACTTAAICTTGTTTCTTCCTACGGTATAAATAT 1697
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                                                                                                                                                                                                                                                                                              Similarity
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antianthritic; antidiabetic; antipsoriatic antiinflammatory; cancer; eye disease; arteriosclerosis; ecute myeloid leukaemia; Alzheimer's disease; AIDS; epile neurofibromatosis; rheumatoid arthritis; participations. Access AIDS; epile gene. Access
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                                                                                        can be used in the diagnosis and treatment of immune system disorders, including eye diseases such as retinopathy, neovascular glaucoma and macular degeneration, arteriosclerosis, anaemia, cancer, acute myeloid leukaemia, Alzheimer's disease, AIDS, epilepsy, neurofibromatosis,
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antirheumatic; antiarthritic; antidiabetic; antipsoriatic;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Buchnera
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ATATTGTTAGTATTCTTTTTTATATTACCAATATATTTATCATCAATTAATATTGGCAAC 324745
                                                                                                                                                                                                                                                                           TCTTCTATCATGTAAAAATAATCAATTTCTTTCTTAATATCAATAATTCTTTTAATATAT
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  AGATACTAGTATGTGATTATTCCAAATACATACTTTGGATGTTTAAACTTAATCTTGTTT 1678
                                                                   TTAATTACCGTATGTTTTTGTTGCCATAATGACAGCCTCTACAACTGTGATAGTCAATTT 1858
                                                                                                                                   GCATGAAGGATAAACCTAATGACTTTAATTTTTTGAAAATGTAACCCTTTTACTCATAGA 1798
                                                                                                                                                                                                                                                                                                                                               CTTCCTACGGTATAAATATTAATCATCGAGGTAAAAAAAGTTTTGTCTTATTTTCGCGAT 1738
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Page 16-230; 237pp; Japanese.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Conservative
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Pred. No.
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WPI; 2002-147896/19
                       Olek A,
                                                                      30-JUN-2000;
01-SEP-2000;
                                                                                                                                                                                   Synthetic.
                                                                                                                                                                                                                                   Human; signal transduction associated gene; cytosine methylation state; 
CpG island; signal transduction associated disease; solid tumour; cance
                                                                                                                                                                                                                                                                     Signal transduction associated gene modified complementary DNA #177.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               2149
                                                                                                          29-JUN-2001; 2001WO-EP07472
                                                                                                                                   03-JAN-2002
                                                                                                                                                          W0200200926-A2
                                                                                                                                                                                             Homo sapiens.
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                                                                                                                                                                                                                                                                                                                      ABK31511;
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                                               (EPIG-)
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                                                                                                                                                                                                                                                                                                                                                                                                                               ATAAATAAAATTTGAGTAAAT
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       EPIGENOMICS
                       Piepenbrock C,
                                                                                                                                                                                                                      signal transduction cytostatic; mutant;
                                                                      2000DE-1032529
2000DE-1043826
                                                                                                                                                                                                                                                                                             (first entry)
                        Berlin
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                                                                                                                                                                                                                      associated disease; solid ds.
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cc signal transduction associated genes. The DNA sequences are chemically condified using a solution of bisulphite, hydrogen sulphite or cdisulphite. Also disclosed are oligonucleotides and/or PNA oligomers compens, and a method for the diagnosis and/or therapy of genetic parameters of genes associated with signal transduction. Cc repigenetic parameters of genes associated with signal transduction. Cc contain DNA, e.g. cell lines, biopsies, blood, sputum, stool, urine, ceyes, intestine, kidney, brain, heart, prostate, lung, breast or liver, cc sequences of the invention are useful for the diagnosis and therapy of sequences of the invention are useful for the diagnosis and therapy of cancer. ABK31159-BBK31545 represent chemically pretreated genomic DNA cc their complementary sequences.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Query Match
                                                                                                                                                                                               1491
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Sequence 47108 BP; 15349 A; 429 C; 8736 G; 22594 T; 0 other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                 853
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 their complementary sequences.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Oligonucleotide for diagnosis and therapy of diseases associated with signal transduction e.g. cancer, comprises chemically modified genomic sequences of genes associated with signal transduction
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              The present invention relates to chemically modified DNA sequences of
TTTATATTAGATACTAGTATGTGATTATTCCAAAT----ACATACTTTGGATGTTTAAA 1665
                                                                    ATATACTTATCTACCTTTTAAAACAAAATACACTAAATTTAATTTAATCTCTTAAATAAC 495
                                                                                                                                                              TTCGAAGTCCTCTACAAGCGTGTAACCATCTGCAACTATTAAATTGCTTTTAATGCA 1550
                                                                                                      TCTTTAACATATTTATTGTTAGTTGGAATTTAATAAGAGCGAACTTGTAACATTACAATA 1610
                                                                                                                                                                                                                                              AACGATTTTTCTTGGATTCCATTCAATGATCTAAAATGCATAGATCTTTTGGGTTACAGT 1490
                                                                                                                                          AAATTATTTTAAAATTAAACACATACACACTAATCTAAAATAACTATAATCCATATAAC-
                                                                                                                                                                                                                                                                                                                                                                                      ATGTGATGTCGATAAATGAAATTCACACGCGTGGTAATAATTATGGGACCGTATGTTACG 1370
                                                                                                                                                                                                                                                                                                                                                                                                                          TATTCTCGAATAATTTAAAAAAAAAATATATACTATTCTTACAACTTCTCTATAAAATTA 794
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ATTATATAAAAAATATTCTTCTTTATAAAAACTATAAAATATACAAATATTTAACAAAT 854
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      The sequence data for this patent did not form part of the printed fication, but was obtained in electronic format directly from the
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        SEQ ID No 354; 24pp; English.
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Pred. No. 0.00094;
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                              TAACAATATTAAAAATATGATGCCTATAATGTATTTCCTATGTTCTTAAAATATTTTT
                                                                   CTAAAATAATAAAAATTCCTATACATAAAATATAATACCTCTATCATTTTACCAACTTC
                                               TTTTATATTTAGTTATAAATACATTATGAACCAATAATAGTTGGTGAATTCAAATATCTC 2085
                                                                                                                                                              TGATAGTCAATTTTTTCTGCAAATATTAAATTAGGAATTCAATGCTACTATCAATAGAAG 1905
                                                                                                          AAACAGCTGAGTATTACATTTTAATTTAAAGACAAAATTTTTGAAAAATGTTATAATTTC 1965
                                                                                                                                                TTTTACTCATAGATTAATTACCGTATGTTTTTGTTGCCATAATGACAGCCTCTACAACTG 1845
                                                                                                                                                                                                                            TTCACTTTTAACCTTTAAAAATTTTTACTTTATTTTTATTTTCTCTCTCAATATCTAATTT 375
                                                                                                                                                                                                                                                TTATTTTCGCGATGCATGAAGGATAAACCTAATGACTTTAATTTTTTGAAAATGTAACCC
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Search completed: March 29, Job time : 2214.58 secs 2003, 18:59:11



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Result
No.
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Maximum Match 100%
Listing first 45 summaries
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Maximum DB seq length: 2000000000
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Perfect score:
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1: /cgn2_6/ptodata/1/ina/5A_COMB.seq:*

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3: /cgn2_6/ptodata/1/ina/6A_COMB.seq:*

4: /cgn2_6/ptodata/1/ina/6B_COMB.seq:*

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6: /cgn2_6/ptodata/1/ina/backfiles1.seq:*
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                 US-08-487-826B-13

US-08-998-416-288

US-08-998-416-133

US-08-998-416-1137

US-09-9416-138-651

US-09-641-638-651

US-09-641-638-651

US-09-641-638-651

US-09-641-638-651

US-09-641-638-651

US-09-641-638-651

US-09-150-741-1

US-09-316-288

US-08-817-926-27

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US-08-948-265-4

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           Sequence 13, Appl Sequence 186, App Sequence 187, Appl Sequence 1137, App Sequence 651, Appli Sequence 651, Appli Sequence 651, Appli Sequence 651, Appli Sequence 27, Appli Sequence 27, Appli Sequence 27, Appli Sequence 27, Appli Sequence 288, Appli Sequence 288, Appli Sequence 1, Appli Sequence 1, Appli Sequence 36, Appli Sequence 1, Appli Sequence 13, Appli Sequence 13, Appli Sequence 13, Appli Sequence 13, Appli Sequence 8, Appli
                                                                                                                                                                                                                                                                                                                                                                                                                                     Description
                                                                                                                                               COUNTAL:

ZIP: 92660

COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/08/487,826B
FILING DATE: 10-SEP-1993
ACTIONING ATTON: 435
ATTORNEY/AGENT INFORMATION:

REGISTRATION NUMBER: 29,655
REFERENCE/DOCKET NUMBER: 39,655
REFERENCE/DOCKET NUMBER: NIH121.001CP1
TELECOMOUNICATION INFORMATION:
TELECHONE: (619) 235-8550
TELECAMOUNICATION OF SEO ID NO: 13:
SEQUENCE CHARACTERISTICS:
LENGTH: 19124 base pairs
                                                   ; ANTI-SENSE: US-08-487-826B-13
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              RESULT 1
US-08-487-826B-13
    Query Match
Best Local Similarity
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Patent No. 5993827
GENERAL INFORMATI
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                                                            STRANDEDNESS:
TOPOLOGY: line
MOLECULE TYPE: (
HYPOTHETICAL: NO
ANTI-SENSE: NO
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APPLICANT: Chitnis, Chetan
APPLICANT: Miller, Louis H.
APPLICANT: Miller, Louis H.
APPLICANT: Peterson, David S.
APPLICANT: Su, Xin-zhaun
APPLICANT: Su, Xin-zhaun
APPLICANT: Wellems, Thomas E.
TITLE OF INVENTION: BINDING DOMAINS FROM PLASMODIUM VIVAX
TITLE OF INVENTION: AND PLASMODIUM FALCIPARUM ERYTHROCYTE BINDING PROTEINS
NUMBER OF SEQUENCES: 45
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    STREET: 6.0 Newport Center Drive 16th Floor STATE: California
COUNTRY: US
ZID: OS
                                                                                                                  LENGTH: 19124 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
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PCT-US-92-00018-1
US-07-638-416-701
US-08-913-842-3
US-08-913-842-6
US-08-913-842-6
US-08-917-951-8673-8
US-08-917-7553-8
US-08-107-7553-8
US-08-617-86018-8
US-08-617-86018-8
US-08-617-86018-8
US-08-617-86018-32
US-08-617-86018-32
Score 77.4; DB 2;
Pred. No. 1.8e-06;
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            Length 19124;
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Patent No. 5231168
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                                    TTTAGTTATAAATACATTATGAACCAATAATAGTTTGGTGAATTCAAATATCTCCATTAAT 2092
                                                                         TGAGTATTACATTTTAATTTAAAGACAAAATTTTTTGAAAAATGTTATAATTTCTAACAAT 1972
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                                                                                                          TTATTTTCAAATACAATTAATTAGATTTCTTAAATATTTCTTCATTTATTCATTTTATA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Patent No.
                                INFORMATION FOR SEQ ID NO: SEQUENCE CHARACTERISTICS: LENGTH: 837 base pairs TYPE: nucleic acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       APPLICANT:
                                                                                                                                                                                                                                                                                                                                                                                                                           ZIP: 27709
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy
                                                                                                                         REGISTRATION NUMBER: 38,241
REFERENCE/DOCKET NUMBER: PF
TELECOMMUNICATION INFORMATION:
TELEPHONE: 919-541-8587
                                                                                                                                                                                             FILING DATE: 31-DEC-1996
ATTORNEY/AGENT INFORMATION:
NAME: Meigs, J. Timothy
                                                                                                                                                                                                                                                                        CLASSIFICATION: 435
PRIOR APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                  CURRENT APPLICATION DATA: US APPLICATION NUMBER: US
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 APPLICANT: Rebischung, Corinne
TITLE OF INVENTION: GENOMIC DNA SEQUENCES OF ASHBYA GOSSYPII
TITLE OF INVENTION: AND USES THEREOF
NUMBER OF SEQUENCES: 1152
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                                                                                                                                                                                                                                                                                                                                                                       SOFTWARE: PatentIn Release #1.0, Version #1.30
                                                                                                                                                                                                                                                                                                                                                                                        COMPUTER: IBM PC compatible OPERATING SYSTEM: PC-DOS/MS-DOS
               STRANDEDNESS:
                                                                                                                                                                                                                                                         APPLICATION NUMBER: CH 0016/97
                                                                                                                                                                                                                                                                                                                   FILING DATE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      STATE:
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o. 6239264
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Research Triangle Park
: No. 6239264th Carolina
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Pohlmann, Rainer
Steiner, Sabine
Mohr, Christine
                                                                                                            919-541-8689
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       USA
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Knechtle, Philipp
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RESULT 3
US-08-487-826B-13/c
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                                                                                                                                                                                                                                                                                  Sequence 13,
Patent No. 5
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Query Match
Best Local Similarity
                                                                                                                                                                                                                                                                       GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Matches
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0,
CURRENT APPLICATION DATA:
                                                                                                                                                            APPLICANT: Wellems, Thomas E.

TITLE OF INVENTION: BINDING DOMAINS FROM PLASMODIUM VIVAX
TITLE OF INVENTION: AND PLASMODIUM FALCIPARUM ERYTHROCYTE
NUMBER OF SEQUENCES: 45
                                                                                                                                                                                                                                                APPLICANT:
APPLICANT:
                                                                                                                                               CORRESPONDENCE ADDRESS:
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ORIGINAL SOURCE:
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                                                                                        COUNTRY:
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                                                                                                                                      ADDRESSEE:
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                                                                             92660
                                                                                                F: 620 Newport Center Drive
Newport Beach
California
                                                                                                                                                                                                                                                                                   3, Application US/08487826B
5993827
                                                                                                                                                                                                                                Sim, Kim L.
Chitnis, Chetan
Miller, Louis H.
                                                                                                                                                                                                         Su, Xin-zhaun
                                                                                                                                                                                                                      Peterson, David S.
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                                                                                                                                  Knobbe Martens Olson & Bear
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Pred. No. 4.6e-05;
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            Version #1,25
                                                                                                                       16th Floor
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Best Local
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INFORMATION FOR SEQ ID NO:
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HYPOTHETICAL: N
ANTI-SENSE: NO
6387 TATTTTTTATGTATTTCATGCATTTTATGAATTTCAAAATTTTATTGTATÄATATAAAA
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                                                                 6444
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LENGTH: 19124 base pairs
TYPE: nucleic acid
                                                                                                                                                                                                                897
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             APPLICATION NUMBER: US/00
FILING DATE: 10-SEP-1993
CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            480 CCAATTAAAATTTCGAATTCATATCTCTTGATTATTAAATTAAATACGAGTGTGAATATC 539
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             420 TAGGTTTATTTGATCATAATTACATGCATCATTTCTTTGATTACTATGAAGATTTTCTTA 479
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            540 CGTTTATCGATCACTCCAATCATGATTATGATTCTTGTGCTAATCCAGCAAATTATTAAC 599
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Local Similarity
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         REFERENCE/DOCKET NUMBER:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         TELEPHONE:
                          AAGCTATTTATACAAAGTTACAAACTGAATATAGCTTGAAATCCTTTAGAAAATTTTTGGA 1136
                                                                                                               ATTATTATATTATATTATTATTATTAATAAAAAATGTTTTTATCATT---TGTTTTGTTG
                                                                                  AATACGATTTTACAGCGTCACTAGTTGAGATTACTAGCATAAAGCATAAAGGACCCGTTC 1076
                                                                                                                                        TGGGACCATTTTGAATAAACTTTTTCTCAAACATTACGGGACACTGGACTCGACCCCTTAA 1016
                                                                                                                                                                         ATCATATTTATATATTCATATATATATAATTGATATAGATACATATTCTTTGTATTGTTG 6565
                                                                                                                                                                                                                                                                                                              AAAATTTGCGATAACGATTGTGAAAAAATATTTTATTTGTTAGCTGATCTCAATATTATGT
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                CTCTTAACTATATTATCGCGGATATATGATAACAATGATATATCACAAAACAATTGTC 956
                                                                                                                                                                                                                                                             AAAAATACGAAAATACAAACATATAAAAAAGTATATATGCAACGTGTTTATATATTTAAT
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Pred. No. 0.00016;
0; Mismatches 1091;
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2208 AACAGATAGAAAACTATTTTGTTGTGGAATGGAAGTAGTAATATACATTAAGCAAATTTT 2267
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                                                          GACTTATTATTCAGTATTCTTATTTATTTTTTTTTTTCCTTATTAAGATTAAAATAA
                                                                                                                                                                                                                                     ---ATATTTTTTGAAATCTACAAATTATTAATATTTAGTCAATAACAATGCATAGAAAGT 2147
                                                                                                                                                                                                                                                                                                                                                          TTAGTTATAAATACATTATGAACCAATAATAGTTGGTGAATTCAAATATCTCCATTA---
                                                                                                                                                                                                                                                                                                                                                                                                                     ATAGATTAATTACCGTATGTTTTTGTTGCCATAATGACAGCCTCTACAACTGTGATAGTC 1853
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                TGTTTCTTCCTACGGTATAAATATTAATCATCGAGGTAAAAAAAGTTTTGTCTTATTTTC 1733
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ATATTAGATACTAGTATGTGATTATTCCAAATACATACTTTGGATGTTTAAACTTAATCT 1673
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                                                                                                                  TTTCTATAATACATGTTACGTATTTGTAATTATGTTACATTTTTAAAAAATGTATAATAT 5382
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ---TATTTAAATATTTTTCAAAAAACTAATCATGTTAATATAATAATAATAAAAT
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                                                                                                                                US-08-998-416-186
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US-08-998-416-186
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                                                                             Query Match
Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Patent No.
                                                                 Matches
                                                                                                                                                                                                                                            TELEFAX: 919-541-8689
INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS:
LENGTH: 615 base pairs
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                              FILING DATE: 24-DEC-1997
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: CH 001
FILING DATE: 31-DEC-1996
ATTORNEY/AGENT INFORMATION:
                    1.750 AAACCTAATGACTTTAATTTTTTGAAAATGTAACCCTTTTACTCATAGATTAATTTACCGT 1809
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APPLICANT: I
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APPLICANT: I
                                                                                                                                                               MOLECULE TYPE:
ORIGINAL SOURCE:
                                                                                                                                                                                                                                                                                                               REFERENCE/DOCKET NUMBER: PF
TELECOMMUNICATION INFORMATION:
TELEPHONE: 919-541-8587
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            APPLICANT: Rebischung, Corinne
TITLE OF INVENTION: GENOMIC DNA SEQUENCES OF ASHBYA GOSSYPII
TITLE OF INVENTION: AND USES THEREOF
NUMBER OF SEQUENCES: 1152
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 5261 TAAGCTATTGGAACTACAAATCAGGATATTTATTTCTTATTTTTCATTTTTTTAAATAA 5202
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                SOFTWARE: PatentIn Release #1.0, Version #1.30 CURRENT APPLICATION DATA:
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CITY: F
 56
                                                                                                                                                                                                              TYPE: nucleion STRANDEDNESS:
                                                                                                                                                 ORGANISM:
                                                                                                                                                                                                   TOPOLOGY:
                                                                                                                                                                                                                                                                                                                                                                 NAME: Meigs, J. Timothy REGISTRATION NUMBER: 38
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  APPLICATION NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  COUNTRY: U
ZIP: 27709
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                STATE:
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TGCATGGTGCGATTCAGAATT 2348
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Research Triangle Park
No. 6239264th Carolina
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Knechtle, Philipp
                                                               Conservative
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Steiner, Sabine
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                                                             0; Mismatches
                                                                             Score 65.8; DB 4;
Pred. No. 0.00015;
                                                                                                                                                                                                                                                                                                                                                   PF/5-30306/A/CGC1976
                                                                                            Length 615,
                                                               Indels
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Patent No. 6239264
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Patent No.
              INFORMATION FOR SEQ ID NO:
                                                                                                                                                                 APPLICATION NUMBER: US
FILING DATE: 24-DEC-19
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
SEQUENCE CHARACTERISTICS:
                                                                         APPLICATION NUMBER: CH 0016/97
FILING DATE: 31-DEC-1996
ATTORNEY/AGENT INFORMATION:
NAME: Meigs, J. Timothy
REGISTRATION NUMBER: 38,241
REFERENCE/DOCKET NUMBER: PF/5-
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APPLICANT:
APPLICANT:
                                            TELECOMMUNICATION INFORMATION: TELEPHONE: 919-541-8587
                                                                                                                                                                                                                                SOFTWARE: PatentIn Release #1.0, Version #1.30 CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                 MEDIUM TYPE: Floppy
                                                                                                                                                                                                                                                                                                                                                                                                                                    TITLE OF INVENTION: GENOMIC DNA SEQUITITLE OF INVENTION: AND USES THEREOF NUMBER OF SEQUENCES: 1152
                                                                                                                                                                                                                                                                                                                                                                                                                          CORRESPONDENCE ADDRESS
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                                                                                                                                                                                                                                                                 MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
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Research Triangle Park
: No. 6239264th Carolina
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                             919-541-8689
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VENTION: GENOMIC DNA SEQUENCES
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Knechtle, Philipp
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Steiner, Sabine
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                                                                       PF/5-30306/A/CGC1976
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RESULT 6
US-09-641-638-651
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                                                                                                                                                                                                                                 Sequence 651, Application US/09641638 Patent No. 6432648
                                                                                                                                                                                                                     GENERAL INFORMATION:
                           TITLE OF INVENTION: BIALLELIC MARKERS DERIVED FROM GENOMIC REGIONS CARRYING TITLE OF INVENTION: GENES INVOLVED IN ARACHIDONIC ACID METABOLISM FILE REFERENCE: GENSET.0510P1
CURRENT APPLICATION UNUMBER: US/09/641;638
CURRENT FILING DATE: 2000-08-16
PRIOR APPLICATION NUMBER: US 09/502,330
PRIOR FILING DATE: 2000-02-11
PRIOR PILING DATE: 2000-02-11
PRIOR PILING DATE: 1999-05-07
                                                                                                                                                             APPLICANT:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Query Match
Best Local Similarity
      PRIOR
                                                                                                                                                                                            APPLICANT:
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TOPOLOGY: line
MOLECULE TYPE: D
ORIGINAL SOURCE:
                                                                                                                                                                                                                                                                                                                                            2380 AACTTTAAAATAAATAAAATTTGAGTAAAT 2410
                                                                                                                                                                                                                                                                                                                                                                                                                                                           2260 CAAATTITAAAAAATTATATAAGCCTATACGCGCTCAAAGTATGTTATCTAGTAGGTGTA 2319
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APPLICATION NUMBER: US 09/275,267 FILING DATE: 1999-03-23
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ORGANISM:
                                                                                                                                                                                                                                                                                                                     TAATTAATATTTATCATTATTTAATTAATT 594
                                                                                                                                                                                                                                                                                                                                                                        ATTAATAATGCATGGTGCGATTCAGAATTGGGACAACAATGAAAACGGAATTAAAATATT 2379
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        TTATTATTTTATTATAATATCTATTTTTATAAATATTATGTTGATTTATATATTTAAT
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Chumakov, Ilya
                                                                                                                                                            Cohen, Annick
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ilarity 47.18;
Conservative
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                        1999-05-07
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Pred. No. 0.00018;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Mismatches
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APPLICATION NUMBER:

us 60/119,917

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PRIOR FILING DATE: 19
NUMBER OF SEQ ID NOS:
SOFTWARE: Patent.pm
SEQ ID NO 651
LENGTH: 20674
                    NAME/KEY: allele
LOCATION: 1827
OTHER INFORMATION: 10-510-173
                                                                    NAME/KEY: allele
LOCATION: 1570
OTHER INFORMATION:
                                                                                                             NAME/KEY: allele
LOCATION: 1559
OTHER INFORMATION: 10-509-284
                                                                                                                                                                                                                                               NAME/KEY: misc_feature
LOCATION: 17555..20674
OTHER INFORMATION: 3'regulatory region
                                                                                                                                                                                                                                                                                              NAME/KEY: exon
LOCATION: 17063..17554
OTHER INFORMATION: exon
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LOCATION: 16775..16945
OTHER INFORMATION: exor
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ORGANISM: Homo sapiens
                                                                                                                                                             OTHER INFORMATION: 10-508-245
                                                                                                                                                                                                                        NAME/KEY: allele
LOCATION: 1128
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LOCATION: 6349..6509
OTHER INFORMATION: exon
                                                                                                                                                                           NAME/KEY: allele
LOCATION: 1182
                                                                                                                                                                                                          OTHER INFORMATION: 10-508-191
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OCATION: 13308..13429
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OCATION: 12854..13023
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LOCATION: 5552
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OCATION: 3124..3297
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OCATION: 16567..16667
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OCATION: 12254..12340
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OCATION: 8645
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NAME/KEY: allele
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OTHER INFORMATION: 10-507-353
NAME/KEY: allele
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LOCATION: 13492
OTHER INFORMATION: 10-507-321
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LOCATION: 12429
OTHER INFORMATION: 10-350-332
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OTHER INFORMATION:
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LOCATION: 8785
OTHER INFORMATION: 10-349-224
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OTHER INFORMATION:
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LOCATION: 8926
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Best Local Similarity 46.8%;
Matches 278; Conservative
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LENGTH: 8920 base pair
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ATTORNEY/AGENT INFORMATION:
NAME: Mitchard, Leonard
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MEDIUM TYPE: Floppy disk
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APPLICATION NUMBER: US
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         FILING DATE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         OPERATING SYSTEM:
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REFERENCE/DOCKET NUMBER: 47
TELECOMMUNICATION INFORMATION:
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2222 TATTTTGTTGTGGAATGGAAGTAGTAATATACATTAAGCAAATTTTAAAAAATTATATAA 2281
                                                                                                                                                                                                                                                                                                                        1993 ATAATGTATTTCCTATGTTCTTAAAATATTTTTTTTTTATATTTAGTTATAATAAAAAATACATTAT
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                                                                                     ACTTCCAAATTTTTTTTTTTTTTGGA----
                                                                                                                                                                                                                                                      GAACCAATAATAGTTGGTGAATTCAAATATCTCCATTAATATTTTTTTGAAATCTACAAAT
                                                                                                                             TATTAATATTTCCAATTAATATGAATACAATTATTAATATTTGATGTGCACACATTA
                                                                                                                                                                                                                                                                                                  Application US/08446855A
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/ENTION: Nucleotide sequence encoding carbamoyl
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SYSTEM: PC-DOS/MS-DOS
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Pred. No. 0.00074;
0; Mismatches 304;
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; SEQ ID NO 1
; LENGTH: 8920
; TYPE: DNA
; ORGANISM: Plasmodium falciparum US-09-150-741-1
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US-09-150-741-1
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CURRENT APPLICATION NUMBER: US/09/150,741
CURRENT FILING DATE: 1998-09-10
EARLIER APPLICATION NUMBER: PL6380
EARLIER FILING DATE: 1992-12-16
EARLIER APPLICATION NUMBER: AU93/00617
EARLIER FILING DATE: 1993-12-02
EARLIER FILING DATE: 1993-12-02
EARLIER APPLICATION NUMBER: 08/446,855
EARLIER APPLICATION NUMBER: 08/446,855
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Best Local Similarity 46.8%;
Matches 278; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                TITLE OF INVENTION: Nucleotide Sequence Encoding Carbamoyl Phosphate Patent No. 6183996
TITLE OF INVENTION: Synthetase II
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                1934 AAGACAAAATTTTTGAAAAATGTTATA-ATTTCTAACAATATTATTAAAAATATGATGCCT 1992
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                                                                                                                                          ACTTCCAAATTTTTTTTTTTTTTTGGA------ACAAGAAATAACAGATAGAAAAC 2221
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                                                                                                                                                                                         TATTAATATTTCCAATTAATATGAATACAATTATTAATATTTTGATGTGTACACATTA 451
                                                                                                                                                                                                                                                                                                                                                                                      Application US/09150741
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Pred. No. 0.00074;
0; Mismatches 304;
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PRIOR APPLICATION NUMBER: US 60/133,200
PRIOR FILING DATE: 199-05-07
PRIOR APPLICATION NUMBER: US 00
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   SEQ ID NO 651
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                CURRENT APPLICATION NUMBER: US/09/641,638 CURRENT FILING DATE: 2000-08-16 PRIOR APPLICATION NUMBER: US 09/502,330 PRIOR FILING DATE: 2000-02-11 PRIOR APPLICATION NUMBER: US 60/133,200 PRIOR FILING DATE: 1999-05-07
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          TITLE OF INVENTION: BIALLELIC MARKERS DERIVED FROM GENOMIC REGIONS CARRYING TITLE OF INVENTION: GENES INVOLVED IN ARACHIDONIC ACID METABOLISM FILE REFERENCE: GENSET.051CP1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    SOFTWARE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      NUMBER OF SEQ ID NOS:
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LOCATION: 3871..4072
OTHER INFORMATION: exon
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LOCATION: 3124..3297
OTHER INFORMATION: exon
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LOCATION: 1123..3123
OTHER_INFORMATION: 5'regulatory region
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TYPE: DNA
ORGANISM: Homo sapiens
                                                     LOCATION: 8645..8854
OTHER INFORMATION: exon
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LOCATION: 5758..5880
OTHER INFORMATION: exon
OTHER INFORMATION: exon
                 NAME/KEY: exon
LOCATION: 12254.
                                                                                          NAME/KEY: exon
                                                                                                         OTHER INFORMATION: exon
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LOCATION: 6349..6509
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LOCATION: 5552
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INFORMATION: exon

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12854..13023

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NAME/KEY: allele
LOCATION: 2947
OTHER INFORMATION: 10-513-365
NAME/KEY: allele
LOCATION: 3802
OTHER INFORMATION: 12-206-81
NAME/KEY: allele
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LOCATION: 1559
OTHER INFORMATION: 10-509-284
NAME/KEY: allele
LOCATION: 1570
OTHER INFORMATION: 10-509-295
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OTHER INFORMATION: 10-343-231
NAME/KEY: almiele
                       OTHER INFORMATION: 10-343-339
                                    NAME/KEY: allele
LOCATION: 4170
                                                            LOCATION: 4109
OTHER INFORMATION: 10-343-278
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OTHER INFORMATION: 12-206-366
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LOCATION: 2934
OTHER INFORMATION: 10-513-352
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LOCATION: 2844
OTHER INFORMATION:
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OTHER INFORMATION: 10-513-250
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OCATION: 2341
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OCATION: 1827
WHER INFORMATION: 10-510-173
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OTHER INFORMATION: 10-508-245
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DIHER INFORMATION: 3'regulatory region
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THER INFORMATION:
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DIHER INFORMATION: exon
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OCATION: 17555..20674
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CATION: 2323
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CATION: 2048
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OTHER INFORMATION: exon
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Query Match
Best Local Similarity
Matches 224; Conserv
                                                  OTHER INFORMATION: NAME/KEY: allele LOCATION: 13535
                                                                                              OTHER INFORMATION:
NAME/KEY: allele
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OTHER INFORMATION:
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OTHER INFORMATION:
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OTHER INFORMATION:
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LOCATION: 8703
OTHER INFORMATION: 10-349-142
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LOCATION: 8608
OTHER INFORMATION: 10-349-47
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LOCATION: 7668
OTHER INFORMATION:
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OTHER INFORMATION:
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LOCATION: 6484
OTHER INFORMATION:
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LOCATION: 8658
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OTHER INFORMATION:
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LOCATION: 6183
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OTHER INFORMATION:
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OTHER INFORMATION:
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LOCATION: 6338
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NAME/KEY: allele
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LOCATION: 6141
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 Score 63; DB 4; Length 20674; Pred. No. 0.0012; 0; Mismatches 230; Indels 1
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MEDIUM TYPE: Floppy disk
COMPUTER: IEM PC compatible
COMPUTER: FC-DOS/MS-DOS
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                                                                                                       SOFTWARE: Patentin Release #1.0, Version CURRENT APPLICATION DATA:
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                                PRIOR APPLICATION DATA:
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APPLICATION NUMBER:
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                                                                                              APPLICATION NUMBER: PCT/
FILING DATE: 12-SEP-1996
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APPLICATION NUMBER: FILING DATE: 29-FE
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Kato, No. 6001590uo
Sakai, Yasuyoshi
                                                                                                                                                                                                                                                                                                                  USA
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Best Local Similarity
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SEQUENCE CHARACTERISTICS:
LENGTH: 4818 base pairs
TYPE: nucleic acid
STRANDEDNESS: double
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ORIGINAL SOURCE:
ORGANISM: Can
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NAME: Bent, Stephen A.
REGISTRATION NUMBER: 29,768
REFERENCE/DOCKET NUMBER: 08
TELECOMMUNICATION INFORMATION:
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             GTAGTAATATACATTAAGCAAATTTTAAAAAATTATAAG
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Pred. No. 0.001;
0; Mismatches 419;
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Best Local Similarity
Matches 209; Conserv
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   1947
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                                                                                                                                                                                                    1767 TTTTTTGAAAATGTAACCCTTTTACTCATAGATTAATTACCGTATGTTTTTGTTGCCATA 1826
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NAME/KEY:
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APPLICATION NUMBER: PCT/AU90/00530
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One Liberty Place 46th Floor
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Chang, Andy C M
Williams, Keith L
WINTION: Improved Plasmid Vectors
VENTION: Slime Moulds of the Genus
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US-09-316-083-2
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US-09-316-083-2
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Best Local Similarity 47.4
Matches 215; Conservative
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SEQ ID NO 2
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EARLIER FILING DATE: 1998-05-22
NUMBER OF SEQ ID NOS: 38
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                                                                                                                           FILING DATE: 1999-05-2
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Pred. No. 0.0014;
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US-08-817-926-27
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US-08-817-926-27/c
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Best Local :
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APPLICANT:
4718 TTTTTTTATTTCTTTTATTTTTTTTTTTTATATATGTCATTTTTGCGTTTATTACAATA 4659
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MEDIUM TYPE: Floppy disk
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APPLICATION NUMBER:
FILING DATE: 12-SEP-
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                        54 TTCTGGTTATTCTGTTCACATGATTTGAGTTTGGTTCTCAATTTGGATTCCAAGATAATT 113
                                                                                                                                                             TOPOLOGY:
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OPERATING SYSTEM: PC-DOS/MS-DOS
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                                                                                                                                                                                                                                                                                                                                                                                                                              APPLICATION NUMBER: PCT/JP96/02597 FILING DATE: 12-SEP-1996
                                                                                                                                                                                                                                                                                                                                                                                                                                                                      CLASSIFICATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  APPLICATION NUMBER: FILING DATE: 09-MAY
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                                                                                                                                                                                                                                                                                                          REGISTRATION NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       SOFTWARE: PatentIn Release #1.0,
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                                                    Local Similarity 46.3 es 275; Conservative
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(202)672-5399
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VENTION: PROMOTER/TERMINATOR FOR CANDIDA BOIDINII
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Kato, No. 6001590uo
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Pred. No. 0.0023;
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                                                                                                                                                                                     COUNTRY:
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Sequence 288, Application US/08998416
FILING DATE: 31-DEC-1996
ATTORNEY/AGENT INFORMATION:
NAME: Meigs, J. Timothy
                                                                                                                                                               SOFTWARE: PatentIn Release #1.0, CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/998,416
                                                                                                                                                                                                                                 COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                         CLASSIFICATION: 435
PRIOR APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                         CORRESPONDENCE ADDRESS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               NUMBER OF SEQUENCES:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 4298 AAAGGTATATTAAATCACTGTTATTACCATTATAACTCAGAAGAGTGTTAAGTTTAATAC
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                                                                                                                                                                                                                                                                                                                                                                             STREET: 3054 Cornwallis Road
CITY: Research Triangle Park
STATE: No. 6239264th Carolina
                                              APPLICATION NUMBER: CH 0 FILING DATE: 31-DEC-1996
                                                                                                                                            APPLICATION NUMBER: FILING DATE: 24-DE
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                T: Wendland, Jurgen
T: Knechtle, Philip
T: Rebischung, Corinne
INVENTION: GENOMIC DNA SEQUENCES
INVENTION: AND USES THEREOF
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Steiner, Sabine
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RESULT 15
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                                                                                                                                                                                                                                                                GENERAL INFORMATION:
APPLICANT: Stewar
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       COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: 1BM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS:
LENGTH: 837 base pairs
TYPE: nucleic acid
CURRENT APPLICATION DATA:
                                                                                                                                                         NUMBER OF SEQUENCES: 2
CORRESPONDENCE ADDRESS:
ADDRESSEE: Nixon & V
                                                                                                                                                                                           APPLICANT: Flores, Maria V
APPLICANT: O'Sullivan, William J
TITLE OF INVENTION: Nucleotide sequence encoding carbamoyl
TITLE OF INVENTION: phosphate synthetase II
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ORIGINAL SOURCE:
ORGANISM: PAG
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                                                                                                   COUNTRY:
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Local Similarity 49.1%;
hes 191; Conservative
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REFERENCE/DOCKET NUMBER: PF
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TELEFAX: 919-541-8689
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5849573th Glebe Road, 8th Floor
                                                                                                                                                                                                                                                              Thomas S
          Release #1,24
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Best Local Similarity
Matches 163; Conserv
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       8451
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                                                                                                                                      2099 TGAAATCTACAAATTATTAATATTTAGTCAATAACAATGCATAGAAAGTTCCAAAAAAA 2158
                                                                                                                                                                   8631 TATAAAAAATAAATCAATATAAATTAATGATCATATTTAATAAAAACATTTATTAATAT
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ATTORNEY/AGENT INFORMATION:
NAME: Mitchard, Leonard
                                                                                                                                                                                                                                                                                                                                                                                                                                                                            SEQUENCE CHARACTERISTICS:
LENGTH: 8920 base pairs
                                                                                                                                                                                                                                                                                                                                                                                                                        MOLECULE TYPE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               NAME: Mitchard, Leonard C
REGISTRATION NUMBER: 29.009
REFERENCE/DOCKET NUMBER: 47-80
                                                                                                                                                                                                                                                                                                                                                                                                                                      TOPOLOGY:
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AAATACATAAATAAGTAATGTTAAATCGAATTTA 8418
                                                   TATTATATATTACTATTTATATATTATACTTTTCATGTTGTTATGGAATGAAAGTTAAT 8452
                                                                                                             AACTATTTTGTTGTGGAATGGAAGTAGTAATATA 2252
                                                                              TTTTGTTAACAGAAACTTCCAAATTTTTTTTTTTTATGGAACAAGAAATAACAGATAGAA 2218
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Pred. No. 0.0031;
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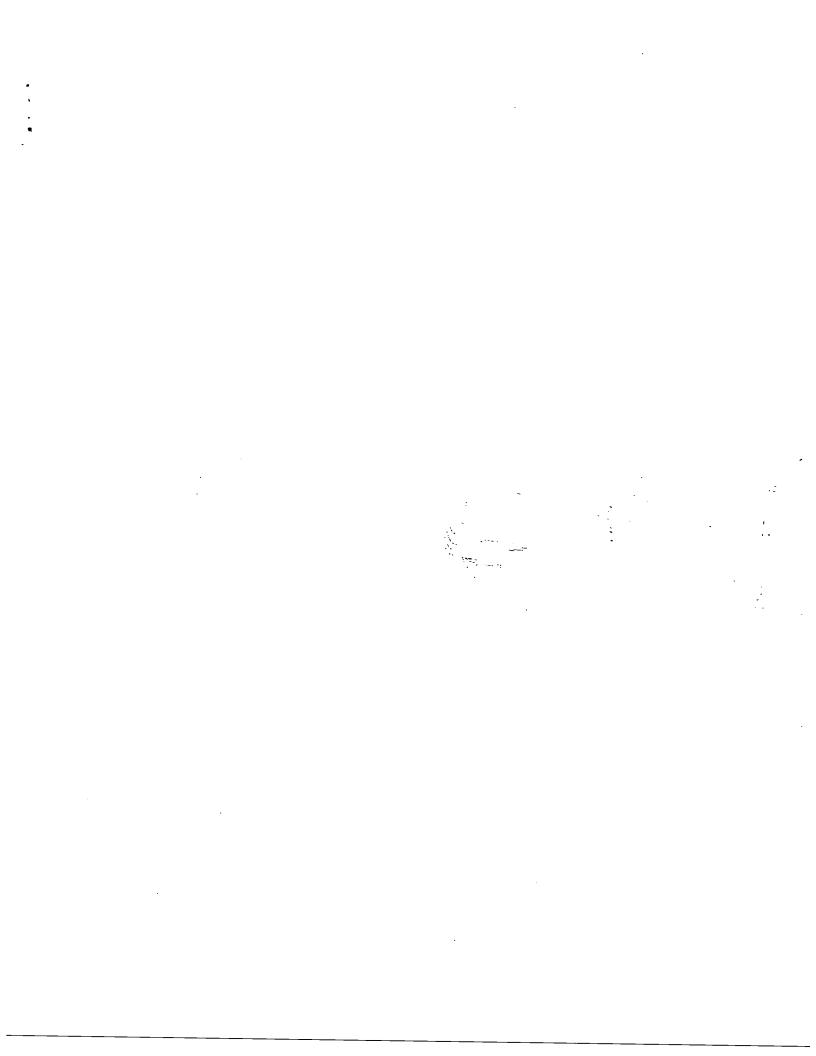
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/cgn2_6/ptodata/1/pubpna/USOB_NEW_PUB.seq:*
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US-10-196-063-1

US-09-938-842A-4756

US-09-774-4114-2

US-09-962-332-154

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US-09-986-352-4582
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Sequence 2, Appli
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Sequence 154, App
Sequence 4, Appli
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Sequence 3, Appli
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Sequence 11234, A
Sequence 1, Appli
Sequence 2, Appli
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Sequence 11218, A
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54	54	54.2	54.6	54.8	54.8	55.2	55.2	55.2	55.6	55.6	55.8	56.2	57	57.2	57.4	57.4	58.4	58.4	58.4	58.6	58.6	59	59.4	59.4	59.8
1.7	1.7	1.7	1.7	1.7	1.7	1.7	1.7	1.7	1.7	1.7	1.7	1.8	1.8	1.8	1.8	1.8	1.8	1.8	1.8	1.8	1.8	1.8	1.9	1.9	1.9
6265	419	1565	416	684973	337	5046	2000	740	53332	53332	2000	1431	2000	2000	513509	414	3272	1109	516	53332	53332	1872	5046	377	302250
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US-09-129-112-3	US-09-960-352-11234	US-09-938-842A-4527	US-09-960-352-4584	US-09-263-959-1	us-09-960-352-6976	US-09-725-735A-13	US-09-938-842A-2868	US-09-791-279-27	US-09-801-861-3	US-10-224-562-3	US-09-938-842A-2991	US-09-774-414-2	US-09-938-842A-3059	US-09-938-842A-3603	US-09-754-853A-4	US-09-960-352-6528	US-09-796-348-18	US-09-938-842A-3333	US-09-960-352-5785	US-09-801-861-3	US-10-224-562-3	US-09-938-842A-3504	US-09-725-735A-13	US-09-960-352-7419	US-09-962-832-154
Sequence 3, Appli	Secuence 11034 A	7507	Seguence 4584 an	Sequence 1. Appli	Sequence 6976. An	Sequence 13. Appl	Sequence 2868. An	Sequence 27. April	Seguence 3 Appli	Sequence 3. Appli	Sequence 2991. An	Sequence 2. Appli	Sequence 3059. An	Sequence 3603. An	Sequence 4. Appli	Sequence 6528. An	Sequence 18. April	Sequence 3333. An	Sequence 5785. An	Segmence 3 April	Sequence 3. Appli	Sequence 3504 An	Sequence 13. Appl	Sequence 7419. An	Seguence 154 App

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                                                                                                                                                                                                                                                                                                                                                           Matches 395;
                                                                                                                                                                                                                                                                                                                                                                           Query Match
Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                SEQ ID NO 1
LENGTH: 640681
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       GENERAL INFORMATION:
324866 TGTGGGTGTATTTTATGTCTCATTAAAAATCTTAAAATTTTTTTAAAGATTTTTCTTCT 324925
                                                                                                                                                                                                                                                           324686 ATATTGTTAGTATTCTTTTTTATATTACCAATATATTTATCATCAATTAATATTGGCAAC 324745
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                CURRENT APPLICATION NUMBER: US/09/790,988 CURRENT FILING DATE: 2001-02-23 PRIOR APPLICATION NUMBER: JF2000-107160
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             APPLICANT: SHIGENOBU, SHUJI
APPLICANT: WATANABE, HIDEMI
APPLICANT: HATTORI, MASAHIRA
APPLICANT: SAKAKI, YOSHIYUKI
TITLE OF INVENTION: GENOME DNA OF BACTERIAL SYMBIONT OF APHIDS
FILE REFERENCE: 081356/0159
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  PRIOR FILING DATE: 2000-04-07
NUMBER OF SEQ ID NOS: 7
SOFTWARE: Patentin Ver. 2.1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                TYPE: DNA
ORGANISM: Buchnera
                                                                                                                                                                                                                             1619
                                                                                                                                                                                                                                                                                                    1559 ATATTTATTGTTAGTTGGAATTTAATAAGAGCGAACTTGTAACATTACAATATTTATATT 1618
                                         GCATGAAGGATAAACCTAATGACTTTAATTTTTTGAAAATGTAACCCTTTTACTCATAGA 1798
                                                                                                                                                                         AAATCTTTTGTACAAAGAAATAAAATATTATTTTTTTTATCTATAAATCCATTTTTGATC 324805
                                                                                                                                                                                                      AGATACTAGTATGTGATTACTTCCAAATACATACTTTGGATGTTTAAACTTAATCTTGTTT 1678
                                                                                    TCTTCTATCATGTAAAAATAATCAATTTCTTTATTATATATCAATAATTCTTTTAATATAT 324865
                                                                                                                           CTTCCTACGGTATAAATATTAATCATCGAGGTAAAAAAGTTTTGTCTTATTTTCGCGAT 1738
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                                                                                                                                                                                                                                                                                                                                                                             2.5%;
45.8%;
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Pred. No. 0.003
0; Mismatches
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0.0033;
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APPLICANT: Byatt, John C.
APPLICANT: Byatt, John C.
APPLICANT: Mathialagan, Nagappan
TITLE OF INVENTION: NUCLEIC ACID AND OTHER MOLECULES ASSOCIATED WITH LACTATION ITILE OF INVENTION: MUSCLE AND FAT DEPOSITION
TILE REFERENCE: 16511.006/37-21(10298)C
CURRENT APPLICATION NUMBER: US/09/960,352
CURRENT FILING DATE: 2001-09-24
NUMBER OF SEQ ID NOS: 15112
SEQ ID NO 11218
                                                                                                                         TYPE: DNA
ORGANISM: Bos taurus
OTHER INFORMATION: Clone ID: 48-LIB3058-026-Q1-K1-D12
5-09-960-352-11218
                                                                                                                                                                                                                                                                                                                                                                                                                                                        GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Sequence 11218, Application US/09960352 Patent No. US20020137139A1
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       TTAGTTATAAATACATTATGAACCAATAATAGTTGGTGAATTCCAAATATCTCCATTAATA 2093
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ACAGATAGAAAACTATTTTGTTGTGGAATGGAAGTAGTAATATACATTAAGCAAATTTTA 2268
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                                                             Similarity
                                          Conservative
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                                                           2.1%;
                                          0;
                                                           Score 66.4; DB 10; Pred. No. 0.038;
                                        Mismatches
                                        Indels
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                                        Gaps
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FEATURE:

FEATURE:

NAME/KEY: CDS

LOCATION: (45163)..(45314),(45450)..(45509),(46941)..(48763),(48975)..(49573)

OTHER INFORMATION: Clone ID: 240017_region_G3

US-09-754-853A-2
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LENGTH: 335913
                                                                                                                                                                                                                                                                                     Query Match
Best Local Similarity
Matches 399; Conserv
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                                                                                                                                                                                                          279575 ATTAATATAAAAATATTAAAATTATAACATTTTTAAGAAAAATATAACAGTAAATATTAT 279634
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   APPLICANT: Parnell, Laurence D.
APPLICANT: Parsons, Jeremy D.
APPLICANT: Wang, Ming Li
APPLICANT: Wang, Ming Li
TITLE OF INVENTION: Nucleic Acid Molecules And Other Molecules Associated With
TITLE OF INVENTION: Soybean Cyst Nematode Resistance
FILE REFERENCE: 388-10(15810)B
CURRENT APPLICATION NUMBER: US/09/754,853A
CURRENT FILING DATE: 2001-01-05
PRIOR APPLICATION NUMBER: US 60/174,880
PRIOR FILING DATE: 2000-01-07
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    NUMBER OF SEQ ID NOS: 1119
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                                                                                                                                                                                                                                            1582 AATAAGAGCGAACTTGTAACATTACAATATTTATATTAGATACTAGTATGTGATTATTCC 1641
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      368
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AACTGATTTCAAAATAGCTTAGCTTTGATTTTACGGACAGTGGAATCGGGTAAGGACCCA 279754
                                                                                          CATCGAGGTAAAAAAGTTTTGTCTTATTTTCGCGATGCATGAAGGATAAACCTAATGAC 1761
                                                                                                                                TTTAATACAAAAATTCCTCTTTTATTTTTAGTTATTTTTTAAGACAAAGATTAACAT
                                                                                                                                                                     AAATACATACTTTGGATGTTTAAACTTAATCTTGTTTCTTCCTACGGTATAAATATTAAT 1701
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                                                                                                                                                                                                                                                                                     Conservative
                                                                                                                                                                                                                                                                                                     2.0%;
                                                                                                                                                                                                                                                                                                     Score 65.2; DB 9;
Pred. No. 0.67;
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APPLICANT: Hauge, Brian M.

APPLICANT: Parnell, Laurence D.

APPLICANT: Parsons, Jeremy D.

APPLICANT: Parsons, Jeremy D.

TITLE OF INVENTION: Nucleic Acid Molecules And TITLE OF INVENTION: Soybean Cyst Nematode Reserved of the Particles of 10,15810) B

CURRENT APPLICATION NUMBER: US/09/754,853A

CURRENT FILING DATE: 2001-01-05

PRIOR APPLICATION NUMBER: US 60/174,880

NUMBER OF SEQ ID NOS: 1119

SEQ ID NO 3

LENGTH: 335913

TYPE: DNA

COCANICAL STREET MAY
: NAME/KEY: CDS
: LOCATION: (46798)..(48763).(48975)..(49573)
: OTHER INFORMATION: Clone ID: 240017_region_G3
US-09-754-853a-3
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Publication No. US20030005491A1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               280407 TTTAATTACCTGTTAACTAATCAGAA 280432
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                                                                                     ORGANISM: Glycine max
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Best Local Similarity 46.1%;
Matches 399; Conservative
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                            ACTATTGAGGGGCAAAAAAAAGACAA 2446
                                                                                                                                    ATGTTATCTAGTAGGTGTAATTAATAATGCATGCGTGCGATTCAGAATTGGGACAACAATG 2360
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                                                                                                               ATTAGTATTAGATATATTATTTATTATATA-TAAATCTCATATTTTGCATAATAATA
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Pred. No. 0.
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US-09-969-373-1212/c

Sequence 1212, Application US/09969373 Patent No. US20020133852A1 GEMERAL INFORMATION: APPLICANT: Effertz, Roger J.

APPLICANT:

Hauge,

Brian M.

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CURRENT APPLICATION NUMBER: US/09/969,373
CURRENT FILING DATE: 2001-10-02
PRIOR APPLICATION NUMBER: US 09/754,853
PRIOR FILING DATE: 2001-01-05
PRIOR APPLICATION NUMBER: US 09/760,427
PRIOR FILING DATE: 2001-01-13
PRIOR APPLICATION NUMBER: US 09/855,768
PRIOR APPLICATION NUMBER: US 09/855,768
PRIOR FILING DATE: 2001-05-15
PRIOR TILING DATE: 2001-05-15
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                                                                                                                     ; OTHER INFORMATION: Clone ID: 48-LIB3058-052-Q1-K1-D8 US-09-960-352-11234
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                                                         Query Match
Best Local
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SEQ ID NO 11234
                                                                                                                                                                                                                                                                                                                                                                                                                                     GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                         Sequence 11234, Application US/09960352 Patent No. US20020137139A1
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Best Local Similarity 52.2%;
Matches 166; Conservative
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APPLICANT: Mathialagan, Nagappan
TITLE OF INVENTION: NUCLEIC ACID AND OTHER MOLECULES ASSOCIATED WITH LACTATION AND
TITLE OF INVENTION: MUSCLE AND FAT DEPOSITION
FILE REFERENCE: 16511.006/37-21(10298)C
CURRENT APPLICATION NUMBER: US/09/960,352
CURRENT FILING DATE: 2001-09-24
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                                                                                                                                                        LENGTH: 419
TYPE: DNA
ORGANISM: Bos taurus
1842 ACTGTGATAGTCAATTTTTTCTGCAAATATTAAATTAGGAATTCAATGCTACTATCAATA 1901
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                                       al Similarity
189; Conserv
                                       Conservative
                                                     2.0%;
                                     Score 64.2; DB 10;
Pred. No. 0.086;
D; Mismatches 188;
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Db 609388
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LENGTH: 640681
TYPE: DNA
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APPLICANT: SHIGENOBU, SHUJI
APPLICANT: WATANABE, HIDEMI
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Best Local Similarity 46.4%;
Matches 327; Conservative
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APPLICANT: SAKAKI, YOSHIYUKI
TITLE OF INVENTION: GENOME DIA OF BACTERIAL SYMBIONT OF APHIDS
FILE REFERENCE: 081356/0159
CURRENT APPLICATION NUMBER: US/09/790,988
CURRENT FILING DATE: 2001-02-23
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TTAAATTAGGAATTCAATGCTATCAATAGAAGAAACAGCTGAGTATTACATTTTAAT 1930
                                                              TAAAAATTTTTTGATTAGAATATTATTCTAGAAAAATTTAAAATATTTTATATACACA 609329
                                                                                                                                          TATTAAATATTTTTTTTATTAACATTAAACTTGATTTTAATAAGATAAAAATAGAATTTTT 609449
                                                                                                                                                                                                                                                        TAAATATTAATCATCGAGGTAAAAAAGTTTTGTCTTATTTTCGCGATGCATGAAGGATA 1750
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                                                                                                    TGTTTTTTGTTGCCATAATGACAGCCTCTACAACTGTGATAGTCAATTTTTTCTGCAAATA 1870
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Pred. No. 1.2;
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; LOCATION: (45163)..(45314),(45450)..(45509),(46941)..(48763),(48975)..(49573)
; OTHER INFORMATION: Clone ID: 240017_region_G3
US-09-754-853a-2
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APPLICANT: Parsons, Jeremy D.
APPLICANT: Wang, Ming Li
TITLE OF INVENTION: Nucleic Acid Molecules An
TITLE OF INVENTION: Soybean Cyst Nematode Re
FILE REFERENCE: 38-10(1.15810)8
CURRENT APPLICATION NUMBER: US/09/754,853A
CURRENT FILING DATE: 2001-01-05
PRIOR APPLICATION UMBER: US 60/174,880
PRIOR FILING DATE: 2000-01-07
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Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Sequence 2, Application US/09754853A Publication No. US20030005491A1 GENERAL INFORMATION:
NUMBER OF SEQ ID NOS: 1119
SEQ ID NO 2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          APPLICANT: Hauge, Brian M. APPLICANT: Parnell, Laure
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                                                                                                                                                                                                                                                                                                                                                       LENGTH: 335913
TYPE: DNA
ORGANISM: Glycine max
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                                                                                                                                                                1923 АТТТТААТТТАААGACAAAATTTTTGAAAAATGTTATAATTTCTAACAATATTATTAAAA 1982
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                              AATACATTATGAACCAATAATAGTTGGTGAATTCAAATATCTCCATTAATATTTTTTTGAA 2102
                                                                258;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    CTGATGAAACTTTAATTTATTTAAATCTAGCTAAAGAGACTGATGTAAAATCTGGAA 608974
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                                                                                                                                                                                                          Conservative
                                                                                                                                                                                                                           2.0%;
                                                                                                                                                                                                        Score 62.8; DB 9;
Pred. No. 1.7;
0; Mismatches 282;
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; LOCATION: (46798)..(48763),(48975)...(49573)
; OTHER INFORMATION: Clone ID: 240017_region_G3
US-09-754-853A-3
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Best Local Similarity
                                                                                                                                                                                                            Matches 258;
                                                                                                                                                                                                                                                                                                                                                                                                             SEQ ID NO 3
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Sequence 3, Application US/09754853A Publication No. US20030005491A1 GENERAL INFORMATION:
CURRENT APPLICATION NÜMBER: US/09/754,8:
CURRENT FILING DATE: 2001-01-05
PRIOR APPLICATION NUMBER: US 60/174,880
PRIOR FILING DATE: 2000-01-07
NUMBER OF SEQ ID NOS: 1119
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    APPLICANT: Wang, Ming Li
TITLE OF INVENTION: Nucleic Acid Molecules
TITLE OF INVENTION: Soybean Cyst Nematode
FILE REFERENCE: 38-10(15810)B
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APPLICANT: Parnell, Laurence D.
APPLICANT: Parsons, Jeremy D.
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                                                                                              AATACATTATGAACCAATAATAGTTGGTGAATTCCAAATATCTCCATTAATATTTTTTGAA 2102
                                                                                                                             ATTTCTGATTAGTTAACAGGTAATTAAACTCATAACGAATATAATAATAATTATAATAATA 280375
                                                               AGGTTT 279893
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Pred. No. 1.7;
0; Mismatches 282;
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US-09-754-853A-1
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Best Local :
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SEQ ID NO 1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                               CURRENT APPLICATION NUMBER: US/09/754,853A CURRENT FILING DATE: 2001-01-05 PRIOR APPLICATION NUMBER: US 60/174,880 PRIOR FILING DATE: 2000-01-07
                                                                                                                                                                                                                                                                                                                                                                                                                                                                       TITLE OF INVENTION: Nucleic Acid Molecules And Other Molecules Associated With TITLE OF INVENTION: Soybean Cyst Nematode Resistance FILE REFERENCE: 38-10(15810)B
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nes 383; Conserv
AA--ATTATTATTATTTGTTTATATAGATTAAAATTGATCTATATGAATATTTTAAAA 71721
                                                                                                                                               AACGATTTTTCTTGGATTCCATTCAATGATCTAAAATGCATAGATCTTTTGGGTTACAGT 1490
                                                                                                                                                                            ATCATTAAATTCAAAATTCATTTTATATAAATTATATATACAAAATCTAATATTAATCTA 71663
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                                                           TATAAATTATTGATTATTTTTTTTTTTGTTCAATTTTAATAAAATTTGATTCAAATGA 71781
                                                                                     GGGTTT 2466
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                                                                                                                                                                                                                                       Conservative
                                                                                                                                                                                                                                                   1.9%;
43.5%;
                                                                                                                                                                                                                                                   Score 62.2; DB 9; Pred. No. 1.5;
                                                                                                                                                                                                                                      Mismatches 493;
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                                                                            ; TYPE: DNA
; ORGANISM: Tetrahymena thermophila
US-10-196-063-1
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 Query Match
Best Local S
Matches 305
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Publication No. US20030027192A1
GENERAL INFORMATION:
APPLICANT: Gorovsky, Martin A.
                                                                                                                                 NUMBER OF SEQ ID NOS: 1
SOFTWARE: PatentIn Ver. 2.1
SEQ ID NO 1
LENGTH: 3410
                                                                                                                                                                                                                                             CURRENT APPLICATION NUMBER: US/10/196,063
CURRENT FILING DATE: 2002-07-15
PRIOR APPLICATION NUMBER: 60/305,167
PRIOR FILING DATE: 2001-07-13
                                                                                                                                                                                                                                                                                                              APPLICANT: Shang, Yuhua
APPLICANT: Song, Xiaoyuan
TITLE OF INVENTION: TETRAHYMENA METALLOTHIONEIN GENE PROMOTER AND ITS
FILE REFERENCE: 176/61102
                                                                                                                                                                                                              PRIOR APPLICATION NUMBER: 60/317,322 PRIOR FILING DATE: 2001-09-05
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   Local Similarity
nes 305; Conserv
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             AATTATGTATCAAACGACATAAAAAATATGAAGCAGTAAAATTACAAATACTTTATGGCA
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     Conservative
               1.98;
Score 61.6; DB 9;
Pred. No. 0.49;
0; Mismatches 359;
                                     Length 3410;
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PRIOR APPLICATION NUMBER: US 60/227,866
PRIOR FILING DATE: 2000-08-24
PRIOR FILING DATE: 2001-01-16
PRIOR FILING DATE: 2001-01-16
PRIOR APPLICATION NUMBER: US 60/300,111
PRIOR FILING DATE: 2001-06-22
NUMBER OF SEQ ID NOS: 5379
SEQ ID NO 4756
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                                                                                                                                                                                                                                                                                             Sequence 4756, Application US/09938842A Patent No. US20020160378A1 GENERAL INFORMATION:
                                                                                                                                    TITLE OF INVENTION: STRESS-REGULATED GENES OF PLANTS, TRANSGENIC PLANTS CONTAINING TITLE OF INVENTION: SAME, AND METHODS OF USE FILE REFERENCE: SCRIP1300-3

CURRENT APPLICATION NUMBER: US/09/938,842A

CURRENT FILING DATE: 2001-08-24
                                                                                                                                                                                                                         APPLICANT: Harper, Jeff
APPLICANT: Kreps, Joel
APPLICANT: Wang, Xun
APPLICANT: Zhu, Tong
LENGTH: 1713
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US-09-774-414-2
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; ORGANISM: Arabidopsis thaliana
US-09-938-842A-4756
Query Match
Best Local Similarity
Matches 215; Conserv
                                                                                                                                                                                         SEQ ID NO 2
                                                                                                                                                                                                                                                                                                                                                          GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                          Sequence 2, Application US/09774414
Patent No. US20020102231A1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Query Match 1.9%;
Best Local Similarity 46.6%;
Matches 229; Conservative
                                                                                                                                                                                                                        PRIOR APPLICATION NUMBER: 09/306,970 PRIOR FILING DATE: 1999-05-07 NUMBER OF SEQ ID NOS: 38
                                                                                                                                                                                                                                                                        CURRENT APPLICATION NUMBER: US/09/774,414
CURRENT FILING DATE: 2001-01-31
                                                                                                                                                                                                                                                                                                           FILE REFERENCE: PH-651
                                                                                                                                                                                                                                                                                                                       APPLICANT: The Institute of Physical and Chemical Research TITLE OF INVENTION: Endonuclease
                                                                                                                                                      LENGTH: 14
TYPE: DNA
                                                                                                                                                                                                       SOFTWARE: PatentIn
                                                                                       NAME/KEY: CDS
LOCATION: (1)
                                                                                                                                          ORGANISM: Saccharomyces
                                                                                                                          FEATURE:
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                                                                                                                                                                         1431
        Conservative
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                      1.98;
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   Score 61.2; DB 10;
Pred. No. 0.41;
0; Mismatches 238;
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; ORGANISM: Homo sapiens
US-09-962-832-154
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US-09-962-832-154
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NUMBER OF SEQ ID NOS: 259
SOFTWARE: PatentIn version 3.0
SEQ ID NO 154
LENGTH: 302250
TYPE: DAY
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APPLICANT: Ebner, R
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     CURRENT APPLICATION NUMBER: US/09/962,832
CURRENT FILING DATE: 2001-09-25
PRIOR APPLICATION NUMBER: US/60/235,077
PRIOR FILING DATE: 2000-09-25
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               TITLE OF INVENTION: Cancer Gene Determination and Therapeutic Screening Using SignaturiTLE OF INVENTION: Sets
FILE REFERENCE: 689290-74
                                                                                                                   300182
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ATTTAGTCAATAACAATGCATAGAAAGTTCCAAAAAAATTTTGTTAACAGAAACTTCCA 2179
                                       TAATAGTTGGTGAATTCAAATATCTCCATTAATATTTTTTGAAATCTACAAATTATTAAT 2119
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PRIOR FILING DATE: 2000-08-24
PRIOR APPLICATION NUMBER: US 60/264,647
PRIOR FILING DATE: 2001-01-16
PRIOR APPLICATION NUMBER: US 60/300,111
PRIOR FILING DATE: 2001-06-22
NUMBER OF SEQ ID NOS: 5379
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; ORGANISM: Arabidopsis thaliana
US-09-938-842A-3532
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CURRENT APPLICATION NUMBER: US/09/938,842A
CURRENT FILING DATE: 2001-08-24
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APPLICANT: Kreps, Joel
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                                                                                                  ATACATTAAGCAAATTTTAAAAAATTATATAAGCCTATACGCGCTCAAAGTATGTTATCT 2309
                                                                                                                                       GTAATATAATTTAAATTTTTACTATAAAATAAATAAATGTTTTGAAGAGAAATTTATAAT
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AATAAATGATTTTTTTAGTAATTCTTATGTTAAATATTAG 412
                                AGTAGGTGTAATTAATAATGCATGGTGCGATTCAGAATTG 2349
                                                                   TATGAATTTATTTTAAATTAGTATAAATAAATGTTTTAAAGTGAAATTTATTTTAAATTT 572
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Zhu, Tong
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Result
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DEFINITION JOURNAL REFERENCE JOURNAL REFERENCE AUTHORS TITLE REFERENCE AUTHORS TITLE TITLE JOURNAL AUTHORS thale cress.
Arabidopsis thaliana
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
Rosidae; eurosids II; Brassicales; Brassicaceae; Arabidopsis. 3 (bases 1 to 473)
Li,Y., Rosso,M., Strizhov,N. and Weisshaar,B.
Direct Submission Rosso,M., Strizhov,N., Li,Y., Reiss,B., Dekker,K. and Weisshaar,B. A new Arabidopsis thaliana T-DNA mutagenised population (GABI-Kat) for flanking sequence tag based reverse genetics A pipeline for automated high-throughput generation of FSTs (flanking sequence tags) from Arabidopsis thaliana T-DNA transformed lines Strizhov,N., Li,Y., Rosso,M., Viehoever,P., Dekker,K., Saedler,H. Unpublished and Weisshaar, B. genomic survey sequence. AL768954
Arabidopsis thaliana T-DNA flanking Unpublished AL768954.1 GI:21522073 (17-JUN-2002) Weisshaar B., Max-Planck-Institut fuer DNA DNA linear GSS 18-JUN sequence GK-082A08-011867, GSS 18-JUN-2002

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237; Conserv
                                         1 (bases 1 to 148)
Alonso, J.M., Leisse, T.J., Barajas, P., Chen, H., Cheuk, R., Gadrinab
                                                                                          Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; Sosidae; eurosids II; Brassicales; Brassicaceae; Arabidopsis.
                                                                                                                                                                                                                                                                                     BH811044 148 bp DNA linear GSS 02-MAY-20 SALK_057128 Arabidopsis thallana TDNA insertion lines Arabidopsis thallana genomic clone SALK_057128, DNA sequence.
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                                                                                                                                                                    Arabidopsis thaliana
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Location/Qualifiers
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nilarity 70.1%;
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  Karnes,M., Kim,C.J., Parker,H.,
and Ecker,J.R.
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Pred. No. 1.5e-18;
D; Mismatches 101
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                                                                  Rosso,M., Strizhov,N., Li,Y., Reiss,B., Dekker,K. and Weisshaar,B. A new Arabidopsis thaliana T-DNA mutagenised population (GABI-Kat) for flanking sequence tag based reverse genetics
                                                                                                                                                                                        A pipeline for automated high-throughput generation of FSTs (flanking sequence tags) from Arabidopsis thaliana T-DNA transformed lines
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Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
Rosidae; eurosids II; Brassicales; Brassicaceae; Arabidopsis.
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Tel: 858 453 4100 x1752
Fax: 858 558 6379
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                                                                                                                                                                                                                                                                 and Weisshaar, B
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/clone_TSALK_057128"
/clone_Tib="Arabidopsis thaliana TDNA insertion lines"
/clone_Tib="Arabidopsis thaliana lines.
/clone_TPCR was performed on Arabidopsis thaliana lines.
each of which contains one or more TDNA insertion
elements. The resultant fragment for each line was
directly sequenced to determine the genomic sequence at
the site of insertion. Details of the protocols used can
be found at http://signal.salk.edu/tdna_protocols.html"

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Pred. No. 1.4e-11;
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Length 148; Indels

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Dekker, K., Saedler, H.

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RESULT 4
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                                                                                                                                                                              AUTHORS
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                                                                                                                                                                                           Drosophila melanogaster
Drosophila melanogaster
Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;
Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha;
Ephydroidea; Drosophilidae; Drosophila.
                                                                                                                                                                                                                                                                                                                                                                                                AL069706
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    Web: www.genoscope.cns.fr)
    Determination of this BAC-end sequence was carried out as part of a collaboration with the Berkeley Drosophila Genome Project (BDGP).
    The BDGP is constructing a physical map of the Drosophila

                                                                                                 Submitted (02-JUN-1999) Genoscope - Centre BP 191 91006 EVRY cedex - FRANCE (E-mail :
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                                                                                                                                                    Direct Submission
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/clone_lib="Arabidopsis thaliana T-DNA insertion lines"
/clone_lib="Arabidopsis thaliana T-DNA from Arabidopsis thaliana
/note="PCR was performed on DNA from Arabidopsis thaliana
plants (T1) which were transformed with the T-DNA from
vector pAC161. The lines contain one or more T-DNA
insertions. The DNA fragment(s) resulting from the PCR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             processed for submission. T-DNA derived sequences were removed 8 c 70 g 146 t 31 others
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                                                                                                                                                       AAATATTTTTTTATATTAATWAWATTTATAWATTAATATAWWTTWTAAATTWTTAATWTA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         please see http://www.fruitfly.org The BuCp Drosophila melanogaster BAC library was prepared by Kazutoyo Osoegawa and melanogaster BAC library was prepared by Kazutoyo Osoegawa and Aaron Mammoser in Pieter de Jong's laboratory in the Department of Cancer Genetics at the Roswell Park Cancer Institute in Buffalo, NY. The library is named RPCI-98 and was constructed by partial EcoRI digestion of Drosophila DNA provided by the BDGP from the isogenic strain y2; cn bw sp. the same strain used for the BDGP's and how to order individual BAC clones, the entire library, or filters for hybridization from the BACPAC Resource Center can be founded to the training at the training at the training and better can be
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/note="end : T7"
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/db_xref="taxon:7227"
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RESULT 5

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                                                                                              TTTTTGTTGCCATAATGACAGCCTCTACAACTGTGATAGTCAATTTTTTCTGCAAATATT 1872
                                                                                                                                    AATATTAATCATCGAGGTAAAAAAAGTTTTGTCTTATTTTCGCGATGCATGAAGGATAAA 1752
                                                                                                                                                                                                                                                                                           GATTATTCCAAATACATACTTTGGATGTTTAAACTTAATCTTGTTTCTTCCTACGGTATA 1692
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Drosophila melanogaster
Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;
Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha;
Ephydroidea; Drosophilidae; Drosophila.
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/db_xref-"taxon:7227"
/clone-"BACR29B23"
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  1808 GTATGTTTTTGTTGCCATAATGACAGCCTCTACAAC---TGTGATAGTCAATTTTTTCTG 1864
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Query Match
Best Local Similarity
                                                  Determination of this BAC-end sequence was carried out as part of a collaboration with the Berkeley Drosophila Genome Project (BDGP). The BDGP is constructing a physical map of the Drosophila melanogaster genome using these BACs. For further information please see http://www.fruitfly.org The BDGP Drosophila melanogaster BAC library was prepared by Kazutoyo Osoegawa and Aaron Mammoser in Pieter de Jong's laboratory in the Department of Cancer Genetics at the Roswell Park Cancer Institute in Buffalo, NY. The library is named RPCI-98 and was constructed by partial EcoRI digestion of Drosophila DNA provided by the BDGP from the isogenic strain y2; cn bw sp, the same strain used for the BDGP's Pl and EST libraries. A more detailed description of the library and how to order individual BAC clones, the entire library, or filters for hybridization from the BACPAC Resource Center can be found at http://bacpac.med.buffalo.edu/drosophila_bac.htm.
GAACCAATAATAGTTGGTGAATTCAAATATCTCCATTAATATTTTTTTGAAATCTACAAAT 2112
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               TATTAATATTTAGTCAATAACAATGCATAGAAAGTTCCAAAAAAA 2158
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Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;
Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha;
Ephydroidea; Drosophilidae; Drosophila.

[ (bases 1 to 1101)
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    Web : www.genoscope.cns.fr)

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BP 191 91006 EVRY cedex - FRANCE (E-mail : segref@genoscope.cns.fr
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/note="end : TET3"
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/db_xref="taxon:7227"
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Pred. No. 1.
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RESULT 7
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                                                                                                                                                                                                                                             BP 191 9100b EVEX CEUCLA.

- Web: www.genoscope.cns.fr)
- Web: www.genoscope.cns.fr)
- Web: www.genoscope.cns.fr)
- Web: www.genoscope.cns.fr)
- Determination of this BAC-end sequence was carried out as part of a collaboration with the European Drosophila Genome Project (EDGP) - http://www.edgp.ebi.ac.uk - This Drosophila melanogaster BAC library (Dros BAC) was made by Alain Billaud at CEPH (Centre d'Etude du Polymorphisme Humain) with funding provided by a MRC project grant. The DNA was prepared from embryos by Alain Bucheton and Genevieve Payan. It has been constructed in the vector
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Drosophila melanogaster genome survey sequence I/ ELIC C. ...

BACN05N18 of DrosBAC library from Drosophila melanogaster (fruit flv), genomic survey sequence.
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Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygo
Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha;
Ephydroidea; Drosophilidae; Drosophila.
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                                                                              379
                                                                          /note="end
38 c
                                                                                                                                                    /db_xref="taxon:72
/clone="BACN05N18"
                                                                                                               /clone_lib="DrosBAC"
/plasmid="pBeloBAC11"
                                                                                                                                                                      /organism="Drosophila melanogaster'
/db_xref="taxon:7227"
                                                                                                                                                                                                                             Location/Qualifiers
 3.1%;
Score Pred.
                                                                              42
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 98.4;
No. 5.
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 DB 17;
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                 Length 836;
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              Web: www.genoscope.cns.fr)
Determination of this BAC-end sequence was carried out as part of collaboration with the Berkeley Drosophila Genome Project (BDGP)
The BDGP is constructing a physical map of the Drosophila melanogaster genome using these BACs. For further information please see http://www.fruitfly.org The BDGP Drosophila melanogaster BAC library was prepared by Kazutoyo Osoegawa and melanogaster BAC library was prepared by Kazutoyo Osoegawa and Maron Mammoser in Pieter de Jong's laboratory in the Department Cancer Genetics at the Roswell Park Cancer Institute in Buffalo, NY. The library is named RPCI-98 and was constructed by partial
                                                                                                                                                                                                                                                                                     Drosophila melanogaster
Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;
Meoptera; Endopterygota; Diptera; Brachycera; Muscomorpha;
Ephydroidea; Drosophilidae; Drosophila.

1 (bases 1 to 1101)
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Drosophila melanogaster genome survey sequence TET3 end of BAC:
BACR29P01 of RPCI-98 library from Drosophila melanogaster (fruit
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                                                                                                                                                                                                                                                GTAGGTGTAATTAATAAT 2328
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AV717372 DCB Homo sapiens
AV717372
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                                                                         human.
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/db_xref="taxon:7227"
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Liu, F.,
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Qu,J., Zhao,M.,
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Zhou, J.,
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                                                                                                                                                     CAATAATAGTTGGTGAATTCAAATATCTCCATTAATATTTTTTTGAAATCTACAAATTATT 2116
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201203, P. R. China
Tel: 86-21-50801919(ex.45)
Fax: 86-21-50801922
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Contact: Zeguang Han
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clone is available at CHGC
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                                     ATTTTTGAAAAATGTT--ATAATTTCTAACAATATTATTAAAAATATGATGCCTATAATGT 1999
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Bouneau, L., Billault, A.,
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Human gene number estimate provided by genome wide analysis using
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/note="Genoscope sequence ID : COAG222CF06LP1-end : T7"
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/db_xref="taxon:99883"
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                                                                                                                                                                                                                                                      Local
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Determination of this BAC-end sequence was carried out as part of a collaboration with the Berkeley Drosophila Genome Project (BDGP). The BDGP is constructing a physical map of the Drosophila melanogaster genome using these BACs. For further information please see http://www.fruitfly.org The BDGP Drosophila melanogaster BAC library was prepared by Kazutoyo Osoegawa and Aaron Mammoser in Pieter de Jong's laboratory in the Department of Cancer Genetics at the Roswell Park Cancer Institute in Buffalo, NY. The library is named RPCI-98 and was constructed by partial ECORI digestion of Drosophila DNA provided by the BDGP from the 1sogenic strain y2; on bw sp. the same strain used for the BDGP's Pl and EST libraries. A more detailed description of the library or filters for hybridization from the BACPAC Resource Center can be found at http://hacac.mcd.hiffalo.doi.org.
                                                                                                                   ATCATCGAGGTAAAAAAAGTTTTGTCTTATTTTCGCGATGCATGAAGGATAAACCTAATG 1759
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  ATTTAGTCAATAACAATGCATAGAAAGTTCCAAAAAAATTTTGTT
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Location/Qualifiers
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/clone_lib="RPCI-98"
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/db_xref="taxon:7227"
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                                                                                                                                                                                                                                                          Score 94; DB 17;
Pred. No. 0.00021;
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Determination of this BAC-end sequence was carried out as part of a collaboration with the European Drosophila Genome Project (EDGP) - http://www.edgp.ebi.ac.uk - This Drosophila melanogaster BAC library (Dros BAC) was made by Alain Billaud at CEPH (Centre d'Etude du Polymorphisme Humain) with funding provided by a MRC project grant. The DNA was prepared from embryos by Alain Bucheton and Genevieve Payan. It has been constructed in the vector
                                                                                                                                                                                                                                                                                                                          Submitted (23-JUL-1999) Genoscope - Centre National de Sequencage BP 191 91006 EVRY cedex - FRANCE (E-mail : seqref@genoscope.cns.fr - Web : www.genoscope.cns.fr)
                                                                                                                                                                                                                                                                                                                                                                                                                                                   Drosophila melanoĝaster
Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;
Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha;
Ephydroidea; Drosophilidae; Drosophila.
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BACN15M24 of DrosBAC library from
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/organism="Drosophila m
/db_xref="taxon:7227"
/clone=BACN15M24"
/clone_11b="DrosBAC"
/plasmid="pBeloBAC11"
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                                                                                      Drosophila melanogaster
Eukaryota; Metazoa; Arthropoda; Hexapoda; Inse
Reoptera; Endopterygota; Diptera; Brachycera;
Ephydroidea; Drosophilidae; Drosophila.
                                                                                                                                                                                                    Drosophila melanogaster genome survey sequence TET3 end of BAC # BACR08K08 of RPCI-98 library from Drosophila melanogaster (fruit fly), genomic survey sequence.

ALO64001
Submitted (02-JUN-1999) Genoscope - Centre National de Sequencage BP 191 91006 EVRY cedex - FRANCE (E-mail : segref@genoscope.cns.fr - Web : www.genoscope.cns.fr)
                                              Direct Submission
                                                                                                                                                  Drosophila melanogaster.
                                                                          (bases 1 to 1101)
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Drosophila melanogaster
Drosophila melanogaster
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BACR29P01 of RPCI-98 library from
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/note="end : TET3"
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/db_xref="taxon:7227"
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Pred. No. 0.00024;
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Determination of this BAC-end sequence was carried out as part of a collaboration with the Berkeley Drosophila Genome Project (BDGP).

The BDGP is constructing a physical map of the Drosophila melanogaster genome using these BACs. For further information melanogaster BAC library was prepared by Kazutoyo Osoegawa and Aaron Mammoser in Pieter de Jong's laboratory in the Department of NY. The library is named RPCI-98 and was constructed by partial isogenic strain y2; on bw sp. the same strain used for the BDGP's and how to order individual BAC clones, the entire library, or filters for hybridization from the BACPAC Resource Center can be found at hitto. //hachac mad huffalo adu/drosonhila hac htm
AATGWTTTWTAAATTWWGTTAWTTTTTATTTTWAAATTGTATATAAAAAWWATTATGTA
                                    TAACAGAAAACTTCCAAATTTTTTTTTTTTTTATGGAACAAGAAATAACAGATAGAA-----a 2219
                                                                            TWYTTTTWTTTAWITTAAWATTTTTTTAWWTAAWAWTGTAATWAAATTAWWTAAAAW
                                                                                                                                                                                ACTATTTTGTTGGGAATGGAAGTAGTAATATACATTAAGCAAATTTTAAAAAAATTTATATAT 2279
                                                                                                                                                                                                                                       AAWTTAWWTWTTTAAWAWT-----TTAAWTATTAAARWWAATTWAAAAWAAAWTTTWAA 719
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191 91006 EVRY cedex - FRANCE (E-mail : seqref@genoscope.cns.fr
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/organism="Drosophila melanogaster"
/olone="acr2901"
/clone_lib="Repc1-98"
/note="end: TET3"
a 66 c 104 g 351 t 214 ot
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ATTTAAAGACAAAATTTTTGAAAAATGTTATAATTTCTAACAATATTAATAATATGAT 1988
                                                                                                                                                                                                             TATTAAATTAGGAATTCAATGCTACTATCAATAGAAGAAACAGCTGAGTATTACATTTTA 1928
                                                                        TWATTAATATWATTTTTAAAAAAAATWAAAWTTWTTTTAATTWAAATTTTTAAATWTTTT 977
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AL057419
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Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygo
Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha;
Ephydroidea; Drosophilidae; Drosophila.
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/note="end : T7"
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564 ATTAAAARSATAARAAATTAKTRAAAAAATATTTTGTKGTKGTTTTTADTTWDWTTA 506
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                                                                TTTASTSSATAATTATTSVTRATTGVTTDAWTTTAAARSAAAAAAKKTTTRBAAAAAAA 565
                                                                                               CGCGCTCAAAGTATGTTATCTAGTAGGTGTAATTAATAATGCATGGTGCGATTCAGAATT 2348
                                                                                                                                                              TTGTGGAATGGAAGTAGTAATATACATTAAGCAAATTTAAAAAATTATATAAGCCTATA 2288
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REFERENCE AUTHORS		ORGANISM	SOURCE	KEYWORDS	VERSION	ACCESSION		DEFINITION	Locus	AF044216	RESULT 1
1 (bases 1 to 4818) Choe,S., Dilkes,B.P., Fujioka,S., Takatsuto,S., Sakurai,A. and	Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; Rosidae; eurosids II; Brassicales; Brassicaceae; Arabidopsis.	Arabidopsis thaliana	Arabidopsis thaliana.		AF044216.1 GI:2935341	AF044216	complete cds.	Arabidopsis thaliana steroid 22-alpha-hydroxylase (DWF4) gene,	AF044216 4818 bp DNA linear PLN 25-JUN-2001		

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VRKQRTDDDLLGWVLKHSNLSTEQIIDJILSLLFAGHETSSVALALAIFFLQACDKAV
VEKQRTDDDLLGWVLKHSNLSTEQIIDJIKSLLSLEAGHETSSVALALAIFFLQACDKAV
EELREEHLEIARAKKELEGESELWDDYKKMDFTQCVINETLRLGNVVRFLHKKALKDV
RYKGYDIPSGKKVLPVLSAVHLDNSKYDQPNLENPWRQQQNNGASSSGSGSFSTWGN
NYMPFGGGFRLCAGSELAKLEMAVFIHHLVLKFNWELAEDDQPFAFPFVDFPNGLPIR
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GWPFLGETIGYLKPYTATTLGDEMQQHYSKYGKIYRSNLFGEPTIVSADAGLNRFILQ
NEGRLFECSYPRSIGGILGKWSMLVLVGDMHDOMRSISLHELSHARLRFILLKDVFRH
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2562. .2654,2746. .2824,2931. .3040,3795. .4398)
/gene="DWF4"
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/db_xref="GI:2935342"
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/note="member of the cytochrome P450 superfamily;
/codon_start=1
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/gene="DWF4"
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Information on performance of analysis and a more detailed annotation of this entry and other sequences of chromosomes 3, 4 and 5 can be viewed at: http://www.mips.blochem.mpg.de/proj/thal/.
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Rosidae; eurosids II; Brassicales; Brassicaceae; Arabidopsis.
1 (bases 1 to 84196)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                (bases 1 to 84196)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   /note="LTR-t; 7565.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        /note="3
3339...75
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       /product="putative protein"
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/db_xref="G1:656196"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         KEAELEDFFQVAEKDLRNKLLECSMKYNFDFEKDEPLGGGRYEWVKLNP"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  join(12339. .12665,12742. .12803,12888. .13055,13125.
/gene="T3A5.10"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      /organism-"Arabidopsis thaliana"
/variety-"Columbia"
/db_xref-"taxon:3702"
/chromosome-"3"
                                                                                           /gene="T3A5.10"
                                                                                                                                                                                                                                          /gene="T3A5.10"
                                                                                                                                                                                                                                                                                                                                                                              /gene="T3A5.10"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         /codon_start=1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            /note="similarity to cyclin-dependent kinase inhibitor
(ICK1), Arabidopsis thaliana, EMBL:ATU94772_1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        /gene="T3A5.10"
                                                                                                                                                                                       'number=
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        'note="367bp LTR"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ocation/Qualifiers
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.12887
                                                                                                                                              12803
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3, BAC clone T3A5.
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gene CDS

/number=4

codon\_start=1

exon

/number=3

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exon

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/number=3

/number=2

13055

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/ COUNTY CALL CALL
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/ Product = "steroid 23-alpha-hydroxylase (DWF4)"
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RYKGYDIDSGWKLYLFVISAYHLDNSRYDDPOLFNWRWQQQNNGASSGSGSFSTWGN
RYKGYDIPSGWKLYLFVISAYHLDNSRYDDPOLFNWRWQQQNNGASSGSGSGSTSTWGN
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                                                                    complement(26093.
                                                                                                                    NYMPFGGGPRLCAGSELAKLEMAVFIHHLVLKFNWELAEDDKPFAFPFVDFPNGLPIR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  /note="Contains Cytochrome p450 cysteine heme-iron ligand signature AA455-464; Prokaryotic membrane lipoprotein lipid attachment site AA320-330"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   26093. 28999

/gene="73A5.40"

Complement(join(26093. .26338,27091. .27200,27308. .27386,

27478. .27570,27723. .28037,28136. .28288,28374. .28698,

27478. .2999911
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                /translation-"MAYMOTDSGNLMAIAQQLIKQKQQQQSQHQQQEEQEQEPNPWPN PSSFGTILPGSGFSDFFQVTNDPGFHFPHLEHHQNAAVASEEFDSDEWMESLINGGDAS QTNPDFF1YGHDFYSFFSKLSAPSYLMRVNKDDSASQQLPPPPASTAIWSPSPPSPQ HPPPPPPPPPPPPPPLYGHDFYARIHDYARKPETKPDTLIRIKESVSSGDF7QPVGYYFAE ALSHKETESPSSSSSSLEDFILSYKTLNDACDYSKFAHLTANQAILATNOSNNIHI UPGIFFQG1QWSALLQALATRSSGKPTRIRISG1PAPSLGDSPGPSLIATGNRLRDFA ALLDLAFEFYVLTPTQLALATRSSGKPTRIRISG1PAPSLGDSPGPSLIATGNRLRDFA ALLDLAFESTYVTTPTQLALATRSSGKPTRIRISG1PAPSLGDSPGPSLIATGNRLRDFA ALLDLAFETYVTTPTALATGNRLRDFA ALLDLAFA AL
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FGRRIMDLVRSDDDNNKPGTRFGLMEEKEQWRVLMEKAGFEPVKPSNYAVSQAKLLLM
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            complement(18303. .19931)
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/gene="T3A5.30"
complement(18303.
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SLRPILLSSSSFSTKGTWRELLGLKRTHVRSKKTDKVNEEVLSQDHKIISGNVATREC
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/note="similarity to pr
thaliana"
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/gene="T3A5.20"
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/gene="T3A5.10"
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                        al Similarity
357; Conserv
                                                                                                                                                                                                            Conservative
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TDRYSHRYDKMEEDDFRYEREYKRSKRSESREYYR"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     /product="01 snRNP 70K protein"
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VPNWRPRRLGGGLGTSRVGGGEEIVGEQQPQGRTSQSEEPSRPREEREKSREKKKERE
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  complement(join(38307. .38796,38877. .39090,39189.
40180. .40242,40337. .40401,40489. .40564,40655. .40805. .40919,41225. .41323))
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               complement(28779.
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                                                                                                                                                                                                Pred. No. 4.7e

Mismatches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            AACTTTTACTTCGTTTTTGATCCGAAGCAAATAACAAATTGTCAAATACCAAACACAAG
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         TTAGTTCGGGTTTGAGAAAAGGGTTTCGACTTTCGAAAGTGGACGATGTATATAGATTGG
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      2 (bases 1 to 1691)
2 (cheuk,R., Chen,H., Kim,C.J., Koesema,E., Meyers,M.C., Banh,J.,
Cheuk,R., Chaninci,P., Dale,J.M., Goldsmith,A.D., Hayashizaki,Y.,
Bowser,L., Carninci,P.X., Jones,T., Kamiya,A., Karlin-Neumann,G.,
Ishida,J., Jiang,P.X., Jones,T., Kamiya,A., Karlin-Neumann,G.,
Kawai,J., Lam,B., Lee,J.M., Lin,J., Liu,S.X., Miranda,M.,
Kawai,J., Lam,B., Lee,J.M., Jin,J., Liu,S.X., Miranda,M.,
Marusaka,M., Nguyen,M., Onodera,C.S., Paln,C.J., Pham,P.K.,
Quach,H.L., Sakurai,T., Satou,M., Seki,M., Southwick,A., Tang,C.C.,
Toriumi,M., Yamada,K., Yamamura,Y., Yu,G., Yu,S., Shinozaki,K.,
Davis,R.W., Theologis,A. and Ecker,J.R.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      1 (bases 1 to 1691)
1 (bases 1 to 1691)
1 (cheuk, R., Chen, H., Kim, C.J., Koesema, E., Meyers, M.C., Banh, J., Bowser, L., Carninci, P., Dale, J.M., Goldsmith, A. D., Hayashizaki, Y., Ishida, J., Jiang, P.X., Jones, T., Kamiya, A., Karlin-Neumann, G., Kawai, J., Lam, B., Lee, J.M., Lin, J., Liu, S.X., Miranda, M., Marusaka, M., Nguyen, M., Onodera, C.S., Palm, C.J., Pham, P.K., Quach, H.L., Sakurai, T., Satou, M., Seki, M., Southwick, A., Tang, C.C., Toriumi, M., Yamada, K., Yamamura, Y., Yu, G., Yu, S., Shinozaki, K., Yamamura, Y., Tu, G., Yu, S., Shinozaki, K., Yanamura, Y., Tu, G., Yu, S., Shinozaki, K., Yanamura, Y., R., Theologis, A. and Ecker, J.R.
                                                        sequencing and annotation of the RAFL cDNAs: Cheuk,R., Chen,H., Kim,C.J., Koesema,E., Meyers,M.C., Shinn,P., Banh,J. Bowser,L., Dale,J.M., Goldsmith,A.D., Jiang,P.X., Jones,T., Karlin-Neumann,G., Lam,B., Lee,J.M., Lin,J., Liu,S.X., Miranda,M., Nguyen,M., Onodera,C.S., Palm,C.J., Pham,P.K., Quach,H.L., Southwick,A., Tang,C.C., Toriumi,M., Yamada,K., Yamauh,H.L., Southwick,A., Davis,R.W., Theologis,A., and Ecker,J.R.
                                                                                                                                                                                                                                                                                                                      RIKEN Genomic Sciences Center (GSC) members carried out the collection and clustering of RAFL CDNAS (RAFL CDNA: ' RIKEN Arabidopsis Full-Length cDNA'): Seki,M., Narusaka,M., Ishida,J., Satou,M., Kamiya,A., Sakurai,T., Carninci,P., Kawai,J., Hayashizaki,Y. and Shinozaki,K.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Submitted (21-AUG-2001) Salk Institute Genomic Analysis Laboratory (SIGNAL), Plant Biology Laboratory, The Salk Institute for Biological Studies, 10010 N. Torrey Pines Road, La Jolla, CA 92037
                                                                                                                                                                                                                                                          The Salk, Stanford, PGEC (SSP) Consortium members carried out
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; Rosidae; eurosids II; Brassicales; Brassicaceae; Arabidopsis.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Direct Submission
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Arabidopsis thaliana
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Cheuk, R. (SSP/Salk) and Seki, M. (RIKEN GSC) contributed equally to

Conservative

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Mismatches

45;

Indels

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Gaps

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Score 58; Pred. No.

DB 6;

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1691 T 1691
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                                                                                                                                                                                                                                                                                                                                                                                                                                          Sequence 1614 from Pate
AX346543
AX346543.1 GI:18494429
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/protein_id="ALIO5667.1"
/protein_id="ALIO567.1"
/brotein_id="ALIO567.1"
/db_xref="GI:15724348"
/translation="Mretehffllplllipsllsllflllkrrnrktrenlppgks
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APLNLPGTAYHKALOSRATILKFIERKMEERKLDIKEEDQEEEEWKTEDBABMSKSDH
VRKQRTDDDLLGWYLKHSNLSTEQILDILISLLFAGHETSSVAIALAIFFLGRAV
EELREEHLEIARAKKELGESELNWDDYKKMDFTQCVINETLRGNVVRFLHRKALKDV
RXKGYDIFSGWKVLPVISAYHLDNSRYDQPNLENPWRQQQNNGASSSGSGSFSTWGN
RXKGYDIFSGWKVLPVISAYHLDNSRYDQPNLENPWRQQQNNGASSSGSGSGSFSTWGN
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                                                                                           /note="chemically treated genomic DNA (Homo sapiens)"
90 c 1299 g 2914 t
                                                                                                                                                                                 1. .5449
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                                                                                                                                      /organism="synthetic c
/db_xref="taxon:32630"
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/db_xref="taxon:3702"
/chromosome="3"
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                                                                                                                                                                                                                            GATAAATT 3035
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                 TGTTTTGTATTATAAAATTATTTTAGGATTTTTTATTTGTATTTAAAAATAAAATTAT 2907
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Rattus norvegicus clone CH230-29B17,
***, 29 unordered pieces.
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Sequence 1196 from Patent WO0200928.
AX346125
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/note="chemically treated genomic DNA (Homo sapiens)"
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Pred. No. 0.63;
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7, *** SEQUENCING
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                                                                                                                                                                       of Molecular and Human Genetics, Baylor Baylor Plaza, Houston, TX 77030, USA On Jul 12, 2002 this sequence version re Genome Center Genome Center Center: Baylor College of Medicine Center code: BCM
                                                                                                                                                                                                                                                                                                                                                                           Submitted (23-JAN-2002) Human Genome Sequencing Center, Department of Molecular and Human Genetics, Baylor College of Medicine, One Baylor Plaza, Houston, TX 77030, USA
                                                                                                                                                                                                                                                                    Submitted (13-JUL-2002) Human Genome Sequencing Center, Department of Molecular and Human Genetics, Baylor College of Medicine, One
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Direct Submission
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Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae;
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                               Center project name: GNJF
center clone name: CH230-29B17
Summary Statistics
Sequencing vector: plasmid;
                                                                                                      Web site: http://www.hgsc.bcm.tmc.edu/
Contact: hgsc-help@bcm.tmc.edu
Project Information
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              (bases 1 to 173786)
Dye-terminator Big Dye: 100% of reads
                                                                                                                                                                                                                                   replaced gi:18846355
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NOTE: Estimated insert size may differ from sequence length (see http://www.hgsc.bcm.tmc.edu/docs/genbank_draft_data.html).

NOTE: This is a "vorking draft' sequence. It currently consists of 92 contigs. The true order of the pieces is not known and their order in this sequence record is arbitrary. Gaps between the contigs are represented as runs of N, but the exact sizes of the gaps are unknown. This record will be updated with the finished sequence.
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                                                                                                                                                                                                                                         Direct Submission

Direct Submission

Submitted (12-JUL-2002) Human Genome Sequencing Center, Department of Molecular and Human Genetics, Baylor College of Medicine, One Baylor Plaza, Houston, TX 77030, USA
On Jul 11, 2002 this sequence version replaced gi:20066030.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Submitted (24-OCT-2001) Human Genome Sequencing Center, Department of Molecular and Human Genetics, Baylor College of Medicine, One Baylor Plaza, Houston, TX 77030, USA 3 (bases 1 to 309233)
Worley, K.C.
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                                                                    Center project name: CF
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                                                                       CH230-81P10
                                                                                                        CHJV
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(see http://www.hgsc.bom.tmc.edu/docs/Genbank_draft_data.html).

NOTE: This is a 'working draft' sequence. It currently

consists of 61 contigs. The true order of the pieces
is not known and their order in this sequence record is
arbitrary. Gaps between the contigs are represented as
runs of N, but the exact sizes of the gaps are unknown.

This record will be updated with the finished sequence
as soon as it is available and the accession number be preserved.
                                                                                                                                                                                                                                                                       NOTE: Estimated insert size may differ from sequence length
                                                                                                                                                                                                                                                                                                                                          Chemistry: Dye-terminator Big Dye: Assembly program: Phrap; version 0. Consensus quality: 233229 bases at Consensus quality: 233927 bases at Consensus quality: 234451 bases at
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Query Match Best Local Similarity

Score Pred.

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Length 12356;

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Ax251264
                                                                                                                                                                                 artificial sequences.
1 (bases 1 to 12356)
Olek, A., Piepenbrock, C. and Berlin, K.
                                                                                                                                                                                                                         synthetic construct. synthetic construct
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          synthetic construct.
synthetic construct
artificial sequences.
                                                                                                                                                                     Diagnosis of diseases associated with tumor suppressor genes and
                                                                                                                                Epigenomics AG (DE)
                                                                                                                                              Patent:
                                                                                                                                                          oncogenes
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ilarity 48.2%;
Conservative
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                                                                                                                                             WO 0168912-A 232 20-SEP-2001;
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232 from Patent W00168912.
                                                  /organism="synthetic construct"
/db_xref="taxon:32630"
/note="chemically treated genom
68 c 2127 g 6516 t
                                                                                                                   Location/Qualifiers
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/db_xref="taxon:32630"
/note="chemically treated genomic DNA
55 c 1318 g 2991 t
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53.2%;
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Pred. No. 1
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55.6; DB
No. 1.4;
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                                                               sapiens)"
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                                                                       131 TTTGAGAAAAGGGTTTCGACTTTCGAAAGTGGACGATGTATATAGATTGGGAGCTAGGTT 190
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  TTTTTTTTGCCCAATGATATATAAAATTTGGATAAATAATATTATTGGATATTCGTTTT 120
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                                                                                                                                                                                                                                                                                                                                                                                   Center, Stanford University, but call the placed gi:8810447.

94304, USA

On Aug 12, 2000 this sequence version replaced gi:8810447.

* NOTE: This is a 'working draft' sequence. It currently

* consists of 2 contigs. The true order of the places

* is not known and their order in this sequence record is

* is not known and their order the contigs are represented as
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1 (bases 1 to 169546)

Hyman, R. W., Fung, E.L., Qin, F., Rowley, D., J.
Kurdi, O.B., Conway, A.B. and Davis, R.W.
Kurdi, Talciparum 3D7 chromosome 12
                                                                                                                          Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Hyman, R.W., Qin, F., Fung, E.L., Conway, A.B. and Davis, R.W. Direct Submission
                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Submitted (19-FEB-1998) Stanford DNA Sequencing and Technology Center, Stanford University, 855 California Avenue, Palo Alto,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Plasmodium falciparum chromosome 12 clone 3D7, ***
PROGRESS ***, 2 unordered pieces
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Plasmodium
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               AC004157.8 GI:9797712
HTG; HTGS_PHASE1.
                                                                                                                                                                                    69871
                                                                                                                                                                                                                                                                                                                                    arbitrary. Gaps between the contigs are represented as runs of N, but the exact sizes of the gaps are unknown. This record will be updated with the finished sequence as soon as it is available and the accession number will be preserved.
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                                                                                                                                                                           /clone="3D7"
15381 c 15705 g
                                                                                                                                                                                                       Ocrganism="Plasmodium falciparum"
/db_xref="taxon:8833"
/chromosome="12"
/clone="PFYAC293"
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                                                                                                                                                                                                                                                                   .169546
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23666: gap of unknown length
169546: contig of 145880 bp in length
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51.6%;
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/db_xref="taxon:32630"
/note="chemically treated genomic
42 c 1230 g 3849 t
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AX281500 20486 bp Sequence 164 from Patent WO0177376. AX281500

DNA

linear.

PAT

02-NOV-2001

GI:16608755

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                                                 Submitted (04-APR-2002) Genome Analysis, Institute of Molecular Biotechnology, Beutenberstr. 11, Jena 07745, Germany
                                                                                                                                                                                                             Gloeckner,G., Eichinger,L., Szafranski,K., Pachebat,J., Dear,P., Lehmann,R., Baumgart,C., Parra,G., April,J.F., Guigo,R., Kumpf,K Tunggal,B., Cox,E., Quail,M.A., Platzer,M., Rosenthal,A. and
                                                                                                                                                                                                                                                                               Dictyostelium discoideum.
Dictyostelium discoideum
Eukaryota; Mycetozoa; Dictyosteliida; Dictyostelium.
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93491 bp DNA linear HTG 04-APR-2002
Dictyostelium discoideum chromosome 2 map 5401525-5495014 strain
AX4, *** SEQUENCING IN PROGRESS ***, in ordered pieces.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Olek,A., Piepenbrock,C. and Berlin,K. Diagnosis of diseases associated with metastasis Patent: WO 0177376-A 164 18-OCT-2001;
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                                                                                      Direct Submission
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                                                                                                                                                                            Sequence and Analysis of Chromosome 2 of Dictyostelium
                                                                                                                                                                                                Noegel, A.A.
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AC116967.1 GI:19920066
                                                                                                                                                             Unpublished
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(http://genome.imb-jena.de/dictyostelium/)
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/db_xref="taxon:32630"
/note="chemically treated genomic
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Patent: W
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AX344570
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* NOTE: This is a 'working draft' sequence.

* This sequence will be replaced

* by the finished sequence as soon as it is available

* the accession number will be preserved.
                                                                                                                                                                                                                                                                Epigenomics AG
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                                                                                                                                                                                                                                                                            s of known genetic parameter WO 0200932-A 21 03-JAN-2002;
/note="chemically treated genomic DNA (Homo sapiens)-Original length of seq 1: 3.673778 <223>-split as follows -seq 01 0.000.001 TO 0.349.980-seq 02 0.300.001 649.980-seq 03 600.001 TO 0.349.980-seq 05 0.000.001 1.249.980-seq 05 1.200.001 1.549.980-seq 06 2.100.001 1.849.980-seq 07 1.200.001 2.149.980-seq 08 2.100.001 2.449.980-seq 09 2.400.001 2.149.980-seq 10 2.700.001 3.049.980-seq 11 3.000.001 3.349.980-seq 12 3.300.001 3.673.778 <223>-original length of seq 2: 3.673778 <223>-split as follows -seq 14 0.000.001 TO 0.349.980-seq 15 0.300.001 649.980-seq 16
                                                                                                                                                                                                                                                                                                                 Piepenbrock, C. and Berlin, K.
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/strain="AX4"
/db_xref="taxon:44689"
/chromosome="2"
                                                                                                                                                                                             /organism="synthetic construct"
/db_xref="taxon:32630"
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                                                                                                                                                                                                                                                                                                                                                                                                                                          Eukaryota; Mycetozoa; Dictyosteliida; Dictyostelium.

1 (bases 1 to 12328)

Gloeckner.G., Eichinger.L., Szafranski.K., Pachebat.J., Dear.
Lehmann.R., Baumgart.C., Parra.G., April.J.F., Guigo.R., Kumm
Tunggal.B., Cox.E., Quail.M.A., Platzer.M., Rosenthal.A. and
                                                                 Submitted (21-MAY-2002) Genome Analysis, Institute of Molecular Biotechnology, Beutenberstr. 11, Jena 07745, Germany CDS predictions from GeneID may contain errors. Further Information is available from IMB Jena, Department of Genome Analysis
                                                                                                                                                                                                                                  Submitted (06-APR-2002) Genome Analysis, Institute of Molecular Biotechnology, Beutenberstr. 11, Jena 07745, Germany
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Dictyostelium discoideum
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                                                                                                                                                                                                                                                                                                           Baumgart, C.
                                                                                                                                                                                                                                                                                                                                                          The
                                                                                                                                                                                                                                                                                                                                                                                Sequence and Analysis of Chromosome 2 of Dictyostelium Unpublished
                                                                                                                                                                   Direct Submission
                                                                                                                                                                                           Baumgart,C.
                                                                                                                                                                                                                                                                                     Direct Submission
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                                              (http://genome.imb-jena.de/dictyostelium/)
http://www.uni-koeln.de/dictyostelium/project.shtml
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3.673.778"
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to 123280)
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9 1.500.001 1.84
1 2.100.001 2.44
3 2.700.001 3.04
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                                                                                                                                                                                                                                                                                                                                                       Sequencing Consortium
                          Institute for Biochemistry I
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* NOTE: This is a 'working draft' sequence.
* This sequence will be replaced
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QQQQTEDLSNINLNDPISLLAWFTINGIIPQNLSPTEIINVGGIYGQIDLNDLSNVETL
IQQLPHQVLSLIQMNTLDAKIQHLSMISGMPAIIQQESPINKNSSDKSPKDNAYNKRDN
NSYIEDEEFIMMKSHYTEKHKQSKRWYNMEPIRITPLKGHNRAIKAKVESGNSAITVS
TEKKIKFWNLNTGQCIGDYEGESGVLSVEYDHTQKSSCIWPLSDYTKVHIGHKNGTVT
MYDFIEQPIEVIHTSRPTNLADGFDFTFPGKYLIWEHTIIHYMDVETSTLLMNELNAH
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sshergiylskgvaefnispenmyellldissrskmdfhcreahiieeydhlnhiihi
nftnplisnldmnlyrsckydpqerlfviamrsieledgdvdqfeclpngwyiqglrg
qkdkckmtfvqqcdlrdielqripgyksfnskerledfqflflfpatvsgrlakifes
                                                                                                                                                                                      GNSISNNPITNNKPPIHIPFSATSRFERISKESIVKEKLYCFMRNQKYVGHLTLTPYQ
LIFQSIMEPGLIGKSVQLHAEYSHIISCKYLFDKSEWLAHFSKDWYKEQRYIKDKINK
                                                                                                                                                                                                                                                        TTHPLSGGTPLSPISLSSAVPPINSPSLŠPMIGASNNNNNERLRSQSASTNLVSPSID
ILLNCNNSNYNNNNNSGGFTPSGGNRTRSGSIGCKFAEPPALSNNNYIYQLYTVKE
KDTLTGISLGSEMPROVLIQANFLLHSEKLLKEGTOLÆVYKKKNLNLMSEGIIEQPES
LITTSADSIDSLDINNSSSSVSSSSINGSGGIECLSPTNNSNNRGRALSGGSSLNVND
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KFVVIILFPFLYPSAAPSFDIVFSDSTMAITDFKVKLKKKLDKLASQLKDKKKPYLYH
LLALISSFYKSNKSHFPEITNLLDSPTIQKRIPKNVNNQPKKINLNSPYHEGTSGTPV
                                                                                                                                                                                                                                                                                                                                                                                                                       VKVWDVTPPSNLLHRYNIDSTCNIARFLPFVNNDIIGSISSKGSYNDIQFRNAKCSEH
PILSLSGGHKDTILNFDWRTTEVAGGEKQHYVTSIGKDNQFNMWRITNEMIDIFTKED
GPPKLVLPTNIRISQESQDLMNKMLSNELEESTDEEDISNLNKKSPFITGNNNNNNNN
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/note="ORF_ID:dd_03106"
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AFNLDNWNLSNISVVKKPIFNNVIGNIGTTTTTTTTTTTTTTTTTTTTTTTTTLSTTNNTNVPEIPK
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FFGSGETFLFKIYPDFDIFRWTKENDMFIYASHDYISIGGGSMFGLMMDNEFLHGYSG
                                                                                          SHNNIRSLVSSDSLASSFDETFSTTPKLLQDQTKYQFQEKILMTPEIYKKLRHYLPIR
                                                                                                                                        GANKKYLIFPCIYAIIHKDNSIQTLFFRGSDPTSVHTCFSYLKQLIVDSKFSPQTSSP
                                                                                                                                                            GINGSSVGGIGNDNNSKVKSKVKSKKEEEEHDAFIQKEISKLNLMEEEEEMTVTDEIT
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             TKKITQSKIVAQHELSNKGIVFTTSSDKSAKVWDLINGTCINTLVGHSYAVNCIEPIG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             SVQHHCGDVGSHIGTPQVYNAMVENFADILLDEGNKDGNVVSSKNKRKRNKNNENKNN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        FTSFLAAIEVKGYPTPWEEEMVTKMFAARIISNQNSIINHVNKLTGGSEMIRELPVIP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           MWRNTITMRLLQSVKKGPGNFSSVHWRSICSPNYQVADGIEVHYLPTALLNYGLGDGS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               TSGYYMIGKGSFSSRYSPELLADVLYQKNPFEWDTFYDKTKLVESINSSIREVEVHYR
                        PSETFUNTVLSKENDFKPYVVEVWGIN"
                                                                                                                                                                                                                                IRHITSLSWNTQETNLIASASSDCMANIFDIRERTQGSGGISTNFKARSNLSQIAWNP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       IELY ISNNVKDIETKDIRISIMEKAEKEVNEMFGTTNPDYGWKIYLKKLDMEILIKKT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               join(656.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       strain="AX4"
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'codon\_start=1

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                                                                                                                                                                                                                                                                                                                                                                                                                                                                             NNNSNSIDIKSLPPYORGGIAIQTKSIELLKFKŠLNKSMIEPEIIDFDFMKDSRYN
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ALPLLESGTLGTKGHVQVILPYLTESYASQKDPNEKQTPFCTLKSFPTNLDHCIQWSR
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IKINEFCKENDIKFIVPDCYGLGGWVENDFGDEFKVYDKNGEKLKEVFISNISISTQN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    SKIMCWVALDRGLRLADRRSFPAPRDKWTKITQFYGSKALDASTLIMSLYFFMAPSDP
RNLATLEAILKPYEEGGLVANSLYFRYNLTHGHDDHIATDGLDGEEGTFNICTFWLIE
SLTRASVVNKEYLVKARLIFDEMLGYANHLGLFSEEIGIGGEALGNFPQAFTHLSLIS
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DLFPKHLYRVPEDIGKLENELFMGTIFYWQKWLEKCTYKGRWREIVERSALCLKLMTF
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                                                                                                                                                                                                                                                                                                                                                                                                                                             DKFEKFFAINPLELDKFINQPHYLEQLLNSSSSNKISTSRTLSKMMDNFIESWKDCII
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           PNQL1 INCMENH1HGFEENDY IQFKE1 IGMDQLNDQSKKFKINI INSNCFS INLNDNS
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Matches
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57840 AATTGTATGTTTTGATAAAACTTTTTCAACTTTTGGAGATTTACCAGAATTAT 57892
                                                                                               121 TTAGTTCGGGTTTGAGAAAAGGGTTTCGACTTTCGAAAGTGGACGATGTATAT 173
                                                                                                                                           61 TITTTTTTGCCCAATGATATAAAAAATTTGGATAAATAATATTATTGGATATTCGTTTT 120
                                                                                                                                                                                                                   99;
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ALLVDIAAPSQQSLGSSLFSLMLGTGNLLGYMMGSIDLVRMVPFMKTDTRALFTLSIM
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     KLKANEHAPKILSSYSISSSCGNPHHSETSTTPKQPMTTTTTTTASTANSLSSLNTS
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Search completed: March 30, 2003, 08:25:12 Job time: 3888.39 secs

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Maximum DB seq
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Perfect score:
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                                                                                                                                                                                        Score
                                                                         358
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Match
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358
1 aaaaaaaaaaaagatgaaagt.....tgtcaaataccaaacacaag 358
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Maximum Match 100%
Listing first 45 summaries
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                                                                                                                                                                  The present sequence encodes a DWF4 polypeptide. The polypeptide is a cytochrome P450 enzyme that mediates multiple steps in synthesis of brassinosteroids. Specifically, it mediates multiple 22alpha-hydroxylation steps in brassinosteroid biosynthesis. The DWF4 polynucleotide is used for altering the phenotype of a plant. DWF4 polynucleotide is used for altering the phenotype of different organs, and this size reduction is attributable to a defect in cell elongation. The DWF4 polynucleotides and polypeptides can be used in diagnostic
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                                                                               including eye diseases such as retinopathy neovascular glaucoma and macular degeneration, arteriosclerosis, anaemia, cancer, acute myeloleukaemia, Alzheimer's disease, AIDS, epilepsy, neurofibromatosis, rheumatoid arthritis, psoriasis and inflammatory/ulcerative bowel
                                                                                                                                                                                                 The present invention provides a number of human immune system associa genes which are modified by the methylation of cytosines. The sequence can be used in the diagnosis and treatment of immune system disorders,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Human; immune system disease; cytosine methylation; antiasthmatic; antiarteriosclerotic; antiantaemalc; cytostatic; nootropic; neuroprotective; anti-HIV; anticonvulsant; ophthalmological; antirheumatic; antiarthritic; antidiabetic; antipsoriatic;
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                                                                                                                                                                                                                                                                                                                         Claim 1; SEQ ID NO 1614; 32pp + Sequence Listing;
                                                                                                                                                                                                                                                                                                                                                                                                                  Nucleic acid comprising for diagnosis and treatm
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01-SEP-2000;
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                                                                                                                                                                                                                         Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Claim 1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Nucleic acid comprising fragment of chemically modified gene, useful for diagnosis and treatment of diseases associated with abnormal cytosine methylation -
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01-SEP-2000; 2000DE-1043826.
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TTTTGGGTTT 5385
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             GTTCGGGTTT 133
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                                                                                                                                                                                                            7560 BP; 2154 A; 47 C; 1554 G;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        EPIGENOMICS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              SEQ ID NO 1196;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Piepenbrock C,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  system associated gene SEQ ID NO: 1196.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                (first entry)
                                                                                                                                         16.2%;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                rheumatoid arthritis; psoriasis; bowel dis
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 32pp + Sequence Listing; German.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Berlin
                                                                                                                                      Score 58;
Pred. No.
                                                                                                        Pred. No. 0.05
0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ?
                                                                                                                                                              DB
                                                                                                                                                                                                            3805 T;
                                                                                                                                      .053;
                                                                                                                                                      24;
                                                                                                           145;
                                                                                                                                                                                                       0 other;
                                                                                                                                                         Length 7560;
                                                                                                      Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              disease
                                                                                                      4;
                                                                                                Gaps
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밁 Q

Sequence 5926 BP; 1562 A;

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T; 0 other;

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ABL33652
ID ABL3
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        The present invention provides a number of human immune system associated genes which are modified by the methylation of cytosines. The sequences can be used in the diagnosis and treatment of immune system disorders, including eye diseases such as retinopathy, neovascular glaucoma and leukaemia, Alzheimer's disease, AIDS, epilepsy, neurofibromatosis, rheumatoid arthritis, psoriasis and inflammatory/ulcerative bowel diseases. The present sequence is a gene of the invention.
                                                                                                                                                                                                                                                        01ek
                                                                                                                                             Claim 1;
                                                                                                                                                                         cytosine
                                                                                                                                                                                Nucleic acid comprising fraction diagnosis and treatment
                                                                                                                                                                                                                                                                                                                                                                                                                                                             Human; immune system disease; cytosine methylation; antiasthmatic; antiarteriosclerotic; antianaemic; cytostatic; nootropic; neuroprotective; anti-HIV; anticonvulsant; ophthalmological; antirheumatic; antiarthritic; antidiabetic; antipsoriatic; antinflammatory; cancer; eye disease; arteriosclerosis; anaemia; neurofibromatosis; rheumatoid arthritis; psoriasis; bowel disease; neurofibromatosis; rheumatoid arthritis; psoriasis; bowel disease;
                                                                                                                                                                                                                                                                                                      30-JUN-2000; 2000DE-1032529
01-SEP-2000; 2000DE-1043826
                                                                                                                                                                                                                                                                                                                                             02-JUL-2001; 2001WO-EP07537
                                                                                                                                                                                                                                                                                                                                                                            03-JAN-2002.
                                                                                                                                                                                                                                                                              (EPIG-) EPIGENOMICS
                                                                                                                                                                                                                                                                                                                                                                                                      WO200200928-A2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Human immune system associated gene SEQ ID NO: 1625
                                                                                                                                                                                                                                                                                                                                                                                                                                Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            26-MAR-2002
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ABL33652;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    3028
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ABL33652 standard;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               2908 TATTATTAAATTAATTTGATAAATAGTAATAAATGTGTGTGATGTTATTTTTAAATTT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 2848
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       2788
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       182
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           122
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 62
                                                                                                                                                                                                                        2002-130909/17.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         GACAACTT 305
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         GATAAATT 3035
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       AGCTAGGTTGAGTCTTTGGACATTTGTATTGGATGT----TGTTGATTATTAGTGTCGAC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             TAGTTCGGGTTTGAGAAAAGGGTTTCGACTTTCGAAAGTGGACGATGTATATAGATTGGG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ACTATTAAACCTTAAATGGGCTTTCTATAAGGCCCAATTATATAACGATTATAACAAAGT 297
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        TTTTATTGTGGAGTTATTTTAAATTTTTAAGGATAATTTTATTTTTATGTCGTGTTATTT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        TTTTTTTGCCCAATGATATAAAAATTTGGATAAAAATAATAATATTATTGGATATTTT
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                                                                                                                                  SEQ ID NO 1625; 32pp + Sequence Listing; German.
                                                                                                                                                                      methylation
                                                                                                                                                                                                                                                  Piepenbrock C,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         (first entry)
                                                                                                                                                                                                                                                                              ĀG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             DNA; 5926
                                                                                                                                                                          fragment of chemically modified ment of diseases associated with
                                                                                                                                                                                                                                                 Berlin
                                                                                                                                                                                                                                                 7,
                                                                                                                                                                           gene, us
                                                                                                                                                                                       useful
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DB 24;

Length 5926;

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RESULT 5
AAS46510
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Best Local s
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Matches 159;
                                                                                                                                                                                                06-APR-2000;
07-APR-2000;
30-JUN-2000;
                                                                                                                                                                                                                                                                                                                                                Human; tumour suppressor gene; oncogene; antitumour; cytostatic; cancer; tumour; CpG dinucleotide; single-nucleotide polymorphism; cytosine methylation; ds.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         3471
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      3411
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        3171
              The invention relates to
                                                               analysing
                                                                                 Fragments of chemically modified genes associated with tumour suppressor genes and oncogenes, useful in designing primers and probes for
                                     Claim
                                                                                                                                                                                                                                                         15-MAR-2001;
                                                                                                                                                                                                                                                                                                       WO200168912-A2
                                                                                                                                                                                                                                                                                                                            Homo sapiens.
                                                                                                                                                                                                                                                                                                                                                                                              Tumour suppressor gene derived
                                                                                                                                                                                                                                                                                                                                                                                                                                                                 AAS46510
                                                                                                                                                                 (EPIG-)
                                                                                                                                                                                                                                   15-MAR-2000;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         184
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   2001-602752/68
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        TATATTTGATTTTTGAATGTATTTAATAA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             TTTTACTTCGTTTTTGATCCGAAGCAATAA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     TTAACGAAAGTTGGGTTGGAGGATTGGGTAGGTAGCGTTGGAAAGTATGTTAGTAT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 CTAGGTTGAGTCTTTGGACATTTGTATTGGATGTTGTTGATTAGTGTCGACACTATT. 243
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               TATGAGATATTAAGTTTAGGTTTTAGGAAGAAGATTTTTGGAATGGAAATATTTTTGGGTG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    GTTCGGGTTTGAGAAAAGGGTTTCGACTTTCGAAAGTGGACGATGTATATAGATTGGGAG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           TTTGAAATGGTTATTTATAGAGTTTTTGTTTTTGGGATTTTTAGGAAATTAATATTTAT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                TTTTTGCCCCAATGATATAAAAATTTGGATAAATAATATTATTGGATATTCGTTTTTTA 123
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           AAACCTTAAATGGGCTTTCTATAAGGCCCCAATTATATTACGATTATAACAAAGTGACAAC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       :
                                                                                                                                                                EPIGENOMICS AG
                                  SEQ ID No 232; 27pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                 standard;
                                                                                                                                         Piepenbrock
                                                                      diseases
                                                                                                                                                                                    2000DE-1013847.
2000DE-1019058.
2000DE-1019173.
2000DE-1032529.
2000DE-1043826.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Conservative
                                                                                                                                                                                                                                                         2001WO-EP02955
                                                                                                                                                                                                                                                                                                                                                                                                                   (first entry)
                                                                     s, useful in designing primers and probes for
associated with cytosine methylation state e
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             15.8%;
                                                                                                                                          ó
                                                                                                                                                                                                                                                                                                                                                                                                                                                                  12356
  a nucleic acid comprising a hemically pretreated DNA (CP
                                                                                                                                          Berlin
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Score
Pred.
                                                                                                                                                                                                                                                                                                                                                                                              chemically modified sequence #232
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ed. No. 0.1;
Mismatches 171;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              56.4;
No. 0.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         3500
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sequence of 18 DNA) e.g. with
                                                                     state e.g
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  0;
                                                                                                                                                                                                                                                                                                                                                              SNP
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WO200200928-A2

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                                                                                                                                                                                                                                                                                                                                                                                                                      RESULT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                          밁
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        oncogenes having a sequence taken from 536 (actually 533 since on numbers 408, 458 and 500 are missing from the sequence listing) sequences (Ss) and sequences complementary to (Ss). The nucleic acid may be a peptide nucleic acid-oligomer (PNA) of at least 9 nucleotides and may form part of a set of probes for detecting the cytosine methylation state and/or single nucleotide polymorphisms and also to be used in an example and tumours. The probes can also be used in a method for ascertaining genetic and/or epigenetic parameters for the diagnosis and acritaining genetic and/or epigenetic parameters for the diagnosis and/or therapy of existing diseases or the predisposition to specific diseases, by analysing cytosine methylations. The parameters may be compared to another set of genetic and/or epigenetic parameters, the differences serving as basis for diagnosis and/or prognosis events which are disadvantageous to patients. The present sequence is one of the 503 genomic sequences derived from tumour suppressor genes and concegenes. Sequences with even numbered Seq ID numbers are the complementary sequence of the corresponding odd numbered sequence (e.g. in laging). ID 536 and ID 535, except for those whose partner sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Query Match
Best Local Sin
Matches 118;
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                                                                                                                     gene;
                                                                                                                                                  antiinflammatory; cancer; eye disease; arteriosclerosis; anaemia; acute myeloid leukaemia; Alzheimer's disease; AIDS; epilepsy;
                                                                                                                                                                                                                                         Human; immune system disease; cytosine methylation; antiasthmatic;
                                                                                                                                                                                                                                                                                                                  26-MAR-2002
                                                                                                                                                                                                                                                                                                                                                                                     ABL32028 standard;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Sequence 12356 BP;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            of the printed specification, but was obtained format directly from WIPO at
                                                                                     Homo
                                                                                                                                      neurofibromatosis;
                                                                                                                                                                                        neuroprotective; anti-HIV; anticonvulsant; ophthalmological;
antirheumatic; antiarthritic; antidiabetic; antipsoriatic;
                                                                                                                                                                                                                           antiarteriosclerotic;
                                                                                                                                                                                                                                                                                                                                                    ABL32028
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ftp.wipo.int/pub/published_pct_sequences
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               is missing).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             191
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         GAGTCTTTGGACATTTGTATTGGATGTTGTTGATTATTAGTG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             CCAATGATATAAAAAATTTGGATAAATAATATTATTGGATATTCGTTTTTTAGTTCGGG
                                                                                                                       S
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           The sequence data for this patent
                                                                                                                                                                                                                                                                            immune system associated gene SEQ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Similarity 53.:
18; Conservative
                                                                                                                                                                                                                                                                                                                (first entry)
                                                                                                                                                                                                                                                                                                                                                                                     DNA;
                                                                                                                                         rheumatoid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        3645 A; 68 C; 2127 G; 6516 T;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   15.5%;
53.2%;
                                                                                                                                                                                                                           antianaemic; cytostatic; nootropic;
                                                                                                                                                                                                                                                                                                                                                                                     7351
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Score 55.6;
Pred. No. 0.
                                                                                                                                    eimer's disease; AIDS; arthritis; psoriasis;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Mismatches 104;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               did not
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bowel dis
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WO200177376-A2
                                                       HOMO sapiens
                                                                                                        cytosine methylation;
                                                                                                                                                                                           Human metastasis associated
                                                                                                                                    Metastasis associated gene;
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                                                                                                                                                                                                                                                        26-MAR-2002
                                                                                                                                                                                                                                                                                                                   ABL34611;
                                                                                                                                                                                                                                                                                                                                                                 ABL34611 standard; DNA;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Nucleic acid comprising fragment of chemically modified for diagnosis and treatment of diseases associated with cytosine methylation \,
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157; Conserv
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 EPIGENOMICS AG
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Pred. No.
                                                                                                                                                                                                                                                                                                                                                                 ВP
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                                                                                                                                                                                        ID NO: 164
                                                                                                                          gene therapy;
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RESULT 8
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Best Local S
Matches 169
Human; immune system disease; cytosine methylation; antiasthe antiarteriosclerotic; antianaemic; cytostatic; nootropic; neuroprotective; anti-HTV; anticonvulsant; ophthalmological; antirhumatic; antiarthritic; antidiabetic; antipsoriatic; antiinflammatory; cancer; eye disease; arteriosclerosis; anae
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                                                                                                                                                                                                                                                                                                                                                                   12016
                                                                                     Human immune system associated gene SEQ ID NO:
                                                                                                                        26-MAR-2002
                                                                                                                                                    ABL34127;
                                                                                                                                                                              ABL34127 standard;
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07-APR-2000;
30-JUN-2000;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                     137
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2000DE-1032529.
2000DE-1043826.
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RESULT 9
ABK28455
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Best Local
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  DNA transcription
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01-SEP-2000;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    acute myeloid leukaemia; Alzheimer's disease; AIDS; epilepsy; neurofibromatosis; rheumatoid arthritis; psoriasis; bowel disease;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              leic acid comprising fragment of chemically modified diagnosis and treatment of diseases associated with
                                                                                                                                                                                                                                                                                                                                GACATTTGTATTGGATGTTGATTATTAGTGTCGACACTATTAAACCTTAAATGGGCT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       TTCTATAAGGCCCAATTATATTACGATTATAACAAAGTGACAACTTTTACTTCGTTTTT 318
                                                                                                                                                                                                                                                                                                         ATGTATATGTTATATATATGTTATGTGTGTGTATATACGTTTTTTGTATAAACGTTTATA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                      TACGTGTAGGTGGATATATTTTTTTTTTTTATATTTTCGTGTATATGTAAATTTTTTGTAT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          TATAAAAATTTGGATAAATAATTATTGGATATTCGTTTTTTAGTTCGGGTTTGAGAAA 139
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  AGGGTTTCGACTTTCGAAAGTGGACGATGTATATAGATTGGGAGCTAGGTTGAGTCTTTG 199
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    146;
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                                                                                                                         standard;
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                                         (first entry)
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2000DE-1043826
associated genomic DNA #165.
                                                                                                                         DNA;
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Pred.
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No. 0.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              gene, useful
abnormal
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DNA transcription associated gene; peptide nucleic acid; PNA-oligomer; PNA; cytosine methylation state; SNP; retroviral infection; gene; ds; single nucleotide polymorphism; adenosine deaminase deficiency; cancer; viral infection; Sezary syndrome; haematological disorder; tuberculosis; immunological disorder; Werner syndrome; developmental disorder; psoriasis; Rieger's syndrome; neurological disorder; erythropolesis; neurodegenerative disorder; Waardenburg syndrome; Niemann-Pick disease; myelodysplastic syndrome; myocardial infarction; hypertension; arthritis; angiogenesis; congenital heart disease; HDR syndrome; gene therapy; polyglutamine disorder; solid tumour.
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WO200192565-A2

06-DEC-2001.

06-APR-2001; 2001WO-EP03973

06-APR-2000; 2000DE-1019058 07-APR-2000; 2000DE-1019173 30-JUN-2000; 2000DE-1032529 01-SEP-2000; 2000DE-1043826

(EPIG-) EPIGENOMICS AG

01ek

Piepenbrock

ú

Berlin

New nucleic acids or oligomers, useful for diagnosing or treating diseases associated with DNA transcription, e.g. immunological disorders, Werner syndrome, psoriasis, myocardial infarction, solitumours or cancer -

Claim SEQ ID No 329; 32pp; English.

The invention relates to a nucleic acid, which comprises a segment of the C chemically pretreated DNA of genes associated with DNA transcription from one of 346 sequences, and an oligomer, in particular an oligonucleotide core peptide nucleic acid (PNA)-oligomer that hybridises to or is identical to the chemically pretreated DNA of genes associated with DNA curve transcription. The set of oligomer probes are useful for detecting the cytosine methylation state and/or single nucleotide polymorphisms (SNPs) in a chemically pretreated genomic DNA. The nucleic acids are useful for disposes ing or treating diseases associated with DNA transcription compared to the methylation status), e.g. ademosine deaminase deficiency, viral infection, retroviral infection, Sezary syndrome, compared the methylation status, e.g. ademosine deaminase compared the methylation status, e.g. ademosine syndrome, compared the methylation status, e.g. ademosine syndrome, neurological disorders, humunological disorders, wearner syndrome, compared the methylation of the sease, myelodysplastic syndrome, myocardial compared to the sease, myelodysplastic syndrome, myocardial compared to the sease, myelodysplastic syndrome, myocardial heart compared to the syndrome, arthritis, polyglutamine disorders, solid tumours or cancer. Sequences ABK28127-ABK28472 represent DNA transcription cascociated genomic DNA molecules of the invention.

CC specification but was obtained in electronic format directly from the curve of the sequence and the sequence of the invention. European Patent Office.

Sequence 7138 BP; 1564 A; 288 C; 1759 G; 3527 T; 0 other

Š 밁 Qy Matches Query Match Best Local 3163 Local w al Similarity 153; Conser Conservative 15.1%; 0 Score 54; Pred. No. Mismatches DB 24; Length 7138; 0.27; 165; 0 Gaps 0

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밁 3223 63 TTTTTTGCCCCAATGATATAAAAATTTGGATAATAATAATATTATTGGATATTCGTTTTTT 122

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RESULT 10
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        The invention relates to a nucleic acid comprising a sequence of 18 bases, of a segment of chemically pretreated DNA (CP DNA) e.g. with bisulphite, of genes associated with tumour suppression and oncogenes having a sequence taken from 536 (actually 533 since numbers 408, 458 and 500 are missing from the sequence listing) sequences (Ss) and sequences complementary to (Ss). The nucleic acid may be a peptide nucleic acid-oligomer (PNA) of at least 9 nucleotides and may form part of a set of probes for detecting the cytosine methylation state and/or single nucleotide polymorphisms and also to be used in an array for analysing diseases associated with CpG dinucleotides e.g. cancers and tumours. The probes can also be used in a method for ascertaining genetic and/or epigenetic parameters for the diagnosis and/or therapy of existing diseases or the predisposition to specific diseases by analysing diseases or the predisposition to specific
                                                                                                                                                                                                                                                     Fragments of chemically modified genes associated with tumour suppressor genes and oncogenes, useful in designing primers and probes for analysing diseases associated with cytosine methylation state e.g.
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07-APR-2000;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Human; tumour suppressor gene; cancer; tumour; CpG dinucleotic cytosine methylation; ds.
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                                                                                                                                                                                                               Claim
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2000DE-1032529.
2000DE-1043826.
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                                                                                                                                                                                                               No 467;
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specific may be
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RESULT 11
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Note: The sequence data for this patent did not of the printed specification, but was obtained i format directly from WIPO at
                   WPI; 2002-171649/22
                                                                                                                                                                                           matrix
                                                                                                                                                                                                   Human; ds; bisulphite;
                                                                                                                                                                                                                                Human DNA for staging
                                                                                                                                                                                                                                                                         ABK33955;
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01-SEP-2000;
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                                                                                                          02-JUL-2001; 2001WO-EP07538
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             TTGCCCAATGATATAAAAATTTGGATAAATATATTATTGGATATTCGTTTTTTAGTT
                                                                                                                                                                                                                                                                                                                                                                 TACTTCGTTTTTGA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             151;
                                                                                                                                                                                         ds; astrocytoma; cytostatic; staging; cysteine methylation;
hite; brain tissue; MALDI; ESI; electron spray mass spectrom
assisted laser desorption/ionization mass spectrometry.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Similarity
                                                         EPIGENOMICS
                                                                                                                                                                                                                                                                                             standard;
                                      Piepenbrock
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Conservative
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                                                                             2000DE-1032529
2000DE-1043826
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 genomic DNA fragments using the array and a polymerase, where the amplificates carry a detectable label. The method further involves identifying methylation status of one or more cytosine positions by reference to one or more data sets. The genomic DNA is chemically treated by using a bisulphite, hydrogen sulphite or disulphite. The amplification or step amplifies DNA which is of particular interest in astrocytoma or brain tissue, based on the specific genomic methylation status of brain tissue, as opposed to background DNA. The amplificates carry a fluorescent label or radionuclide. Optionally, the labels of the amplificates are detachable molecule fragments having a typical mass which are detected in a mass spectrometer. The fragments of chemically pre-treated genomic DNA to be amplified, have a single positive or preferably the amplificates of a better detectability in the mass spectrometer.
                                                                                                                                                                                                                                                                                                                                                                                                                                Matches
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                                                                                                                                                                                                                                                                                                                                             10811
                                                                                                                                                                        10931
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       for determining genetic and/or epigenetic parameters, classification, differentiation, grading, staging, treatment and/or diagnosis of astrocytomas, or the predisposition to astrocytomas by analysing cytosine methylations, involves obtaining a biological sample containing genomic DNA, extracting the genomic DNA, converting cytosine bases which are unmethylated at the 5-position, in the genomic DNA sample, to uracil or another base which is dissimilar to cytosine in terms of hybridisation behaviour, by chemical treatment and amplifying chemically pre-treated
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             acid (or set thereof) of at least 9 nucleotides which hybridises to (1), probes for detecting cytosine methylation or single-nucleotide polymorphisms (SNP) in (I), an array of oligomers or peptide nucleic acids for analysing diseases associated with the methylation states of the CpG dinucleotides of (I). The array is useful
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        samples of the invention.

Note: The sequence data for this patent did not form of the printed specification, but was obtained in eleformat directly from WIPO at
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Preferably, the amplificates or fragments of the amplificates are detected by matrix assisted laser desorption/ionization mass spectrometry (MALDI) or using electron spray mass spectrometry (ESI). The present sequence is one of the chemically pre-treated reference DNA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Sequence 14147 BP; 3621 A; 225 C; 3116 G;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      The invention relates to a nucleic acid comprising a sequence (I least 18 bases in length of a segment of chemically pre-treated DNA which has any one of the sequences of (ABK33919-ABK34032) or complement. Also included are an oligonucleotide or peptide nucl
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         characterisation, classific treatment and/or diagnosis
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Claim
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         astrocytomas
                                                                                                                                                                                                                127
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ftp.wipo.int/pub/published_pct_sequences
                                                                                                                                                                                                                                                                                                   67
                                                                                                                                                                                                                                                                                                                                                                Local Similarity
                                                                                                                                                                                                                                                                                                                                          GGTTGAGTCTTTGGACATTTGTATTGGATGTTGTTGATTATTAGTGTCGACACTATTAAA 246
                                                                                                                                                                                                             CGGGTTTGAGAAAAGGGTTTCGACTTTCGAAAGTGGACGATGTATATAGATTGGGAGCTA 186
                                       CCTTAAATGGGCTTTCTATAAGGCCCCAATTATATTACGATTATAACAAAGTGACAACTTT 306
                                                                                                                                                                    TTGCCCCAATGATATAAAAAATTTGGATAAATAATATTATTGGATATTCGTTTTTTAGTT 126
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                                                                                                                                                                                                                                                                                                                                                                                                                              Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           classification, differentiation, grading, staging, liagnosis of astrocytomas or predisposition to
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                39;
                                                                                                                                                                                                                                                                                                                                                                                                                                                 14.9%;
48.1%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             37pp;
                                                                                                                                                                                                                                                                                                                                                                                                                              0
                                                                                                                                                                                                                                                                                                                                                                                                                           Score 53.2; D
Pred. No. 0.36
0; Mismatches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                 . 36;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             7185 T; 0 other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                   DB 24;
                                                                                                                                                                                                                                                                                                                                                                                                                           163;
                                                                                                                                                                                                                                                                                                                                                                                                                              Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Length 14147;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                orm part
electronic
                                                                                                                                                                                                                                                                                                                                                                                                                           0;
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                                                                                                                                                                                                                                                                                                                                                                                                                         Gaps
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RESULT 12
AAS46670
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     11111 TTATTATTATTTGA 11124
                                                                                                                                                                                                                                                  Fragments
genes and
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06-APR-2000; 2000DE-1019058

07-APR-2000; 2000DE-1019173

30-JUN-2000; 2000DE-1032529

01-SEP-2000; 2000DE-1043826
                                                                                                                                                                                                                     Claim 1;
                                                                                                                                                                                                                                                                                          Olek
                                                                                                                                                                                                                                                                                                                                                                                                                                                                Tumour suppressor gene derived chemically modified sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                   cytosine methylation; ds.
                                                                                                                                                                                                                                                                                                                                                                                                                                          Human; tumour suppressor gene; on cancer; tumour; CpG dinucleotide;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 18-DEC-2001
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                AAS46670;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               AAS46670 standard;
                                                                                                                                                                                                                                                                                                                                                                                     20-SEP-2001
                                                                                                                                                                                                                                                                                                                                                                                                    WO200168912-A2
                                                                                                                                                                                                                                                                                                                                                                                                                    Homo sapiens.
                                                                                                                                                                                                                                                                                                         (EPIG-)
                                                                                                                                                                                                                                                                                                                                                                     15-MAR-2001; 2001WO-EP02955
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    307
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   TACTTCGTTTTTGA
                                                                                                                                                                                                                                                                                                         EPIGENOMICS
                                                                                                                                                                                                                     SEQ
                                                                                                                                                                                                                                                                                         Piepenbrock
                                                                                                                                                                                                                                         of chemically modified genes associated with tumour suppressor oncogenes, useful in designing primers and probes for diseases associated with cytosine methylation state e.g.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                (first entry)
                                                                                                                                                                                                                     ID No 392; 27pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               DNA;
                                                                                                                                                                                                                                                                                      c,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               7261 BP
                                                                                                                                                                                                                                                                                          Berlin
                                                                                                                                                                                                                                                                                                                                                                                                                                                 oncogene; antitumour;
                                                                                                                                                                                                                                                                                                                                                                                                                                          single-nucleotide polymorphism;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                 #392
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SNP;

The invention relates to a nucleic acid comprising a sequence of 18 CC bases, of a segment of chemically pretreated DNA (CP DNA) e.g. with CC bisulphite, of genes associated with tumour suppression and CC oncogenes having a sequence taken from 536 (actually 533 since CC numbers 408, 458 and 500 are missing from the sequence listing) sequences CC (SS) and sequences complementary to (SS). The nucleic acid may be a CC peptide nucleic acid-oligomer (PNA) of at least 9 nucleotides and may CC form part of a set of probes for detecting the cytosine methylation state and/or single nucleotide polymorphisms and also to be used in an CC array for analysing diseases associated with CpG dinucleotides e.g. CC ascertaining genetic and/or epigenetic parameters for the diagnosis and/or therapy of existing diseases or the predisposition to specific CC diseases, by analysing cytosine methylations. The parameters may be CC compared to another set of genetic and/or epigenetic parameters, the CC compared to another set of genetic and/or epigenetic parameters, the CC compared to serving as basis for diagnosis and/or prognosis events which CC are disadvantageous to patients. The present sequence is one of the CC complementary sequences derived from tumour suppressor genes and CC complementary sequence of the corresponding odd numbered sequence (e.g. CC Is mission). ID 536 and ID 535, except for those whose partner sequence Note: The sequence data for this patent did not form part of the printed specification, but was obtained in electro format directly from WIPO at

ftp.wipo.int/pub/published\_pct\_sequences

S

7261

BP;

1862 A; 171 C; 1854 G; 3374 T; 0 other;

Query Match

Local

Similarity

14.8%;

Score 53; Pred. No.

DB 22; Length 7261; 0.41;

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RESULT 13
ABL33138
AC ABL33
XX ABL33
XX ABL33
XX ABL33
XX ABL33
XX Human
XX Human
XX Human
XX Human
XX ABL3
XX
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         뫄
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       including eye diseases such as retinopathy,
                                                                  genes which
                                                                                                                                               Claim 1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                 30-JUN-2000;
01-SEP-2000;
                                                                                                                                                                                          cytosine methylation
                                                                                                                                                                                                       Nucleic acid comprising fragment of chemically modified for diagnosis and treatment of diseases associated with
                                                                                                                                                                                                                                                                                                                                                                                                    (EPIG-)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         02-JUL-2001;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Human; immune system disease; cytosine methylation; antiasthmatic; antiarteriosclerotic; antianaemic; cytostatic; nootropic; neuroprotective; anti-HIV; anticonvulsant; ophthalmological; antirheumatic; antiarthritic; antidiabetic; antipsoriatic;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           W0200200928-A2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Homo sapiens.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           antiinflammatory; cancer; eye disease; arteriosclerosis; acute myeLoid leukaemia; Alzheimer's disease; AIDS; epile neurofibromatosis; rheumatoid arthritis; psoriasis; bowe
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Human immune system associated gene SEQ ID NO: 1111.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          26-MAR-2002
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                     present invention provides a number of human immune system associaes which are modified by the methylation of cytosines. The sequence be used in the diagnosis and treatment of immune system disorders,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           73
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                                                                                                                                                                                                                                                                                               2002-130909/17.
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                                                                                                                                            SEQ ID NO 1111;
                                                                                                                                                                                                                                                                                                                                            Piepenbrock C,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       standard;
                                                                                                                                                                                                                                                                                                                                                                                                                                            2000DE-1032529.
2000DE-1043826
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                                                                                                                                    32pp +
                                                                                                                                                                                                                                                                                                                                            Berlin
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                                                                                                                            Sequence Listing; German
                                                                                                                                                                                                                                                                                                                                         <u>~</u>
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        psoriasis; bowel
neovascular glaucoma and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                125;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              epilepsy
                                                                                                                                                                                                       gene, useful abnormal
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   anaemia;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      disease;
                                                  sequences
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          SSSSS & &
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Query Match
                                                                                     Claim 1; SEQ ID NO 8479; 21pp + Sequence Listing; English
                                                                                                                New isolated nucleic acid detection reagent for detecting 1000 or more genes from Drosophila and for elucidating cell signalling and cell-cel
                                                                                                                                                                        Venter
                                                                                                                                                                                                           23-MAR-2000; 2000US-191637P
11-JUL-2000; 2000US-0614150
                                                                                                                                                                                                                                       23-MAR-2001; 2001WO-US09231
                                                                                                                                                                                           (PEKE ) PE
                                                                                                                                                                                                                                                                                                                                            Drosophila melanogaster genomic polynucleotide SEQ ID NO
                                                                                                                                                                                                                                                                                                                                                                                                                                                             3488
                                                                                                                                                                                                                                                                                                 Drosophila melanogaster.
                                                                                                                                                                                                                                                                                                                     pharmaceutical;
                                                                                                                                                                                                                                                                                 WO200171042-A2
                                                                                                                                                                                                                                                                                                                                Drosophila;
                                                                                                                                                                                                                                                                                                                                                                                         ABL19002;
                                                                                                                                                                                                                                                                                                                                                                                                            ABL19002
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             3308
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 macular degeneration, arteriosclerosis, anaemia, cancer, acute myeloid leukaemia, Alzheimer's disease, AIDS, epilepsy, neurofibromatosis, rheumatoid arthritis, psoriasis and inflammatory/ulcerative bowel diseases. The present sequence is a gene of the invention.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Sequence 5678 BP; 1387 A;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                              216
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     156
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  36 TTTTTTTTTGATAATTTTAAATCATTTTTTTTGCCCAATGATATATAAAAATTTTGGATA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ocal
                                                                                                                                                     2001-656860/75.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                           GTTGTTGATTATTAGTGTCG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          TAATTTTATTATTTTTTTATTATTTTGATTGGGTAATTTTAAATGATTTGTATTTGAG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          AAAGTGGACGATGTATATAGATTGGGAGCTAGGTTGAGTCTTTGGACATTTGTATTGGAT 215
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               TATGTTGATTTTTTTTTTG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 AATAATATTATTGGATATTCGTTTTTTAGTTCGGGTTTGAGAAAAGGGTTTCGACTTTCG
                                                                                                                                                                        JC,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   108;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Similarity
                                                                                                                                                                                                                                                                                                                                                                                                           standard; DNA; 21231
                                                                                                                                                                                           CORP NY
                                                                                                                                                                      Adams M,
                                                                                                                                                                                                                                                                                                                         developmental biology; cell signalling;
                                                                                                                                                                                                                                                                                                                                                                    (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Conservative
                                                                                                                                                                                                                                                                                                                     gene;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        14.7%;
                                                                                                                                                                      PWD,
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Pred. No. 0.44
); Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Score 52.8; DB Pred. No. 0.44;
                                                                                                                                                                                                                                                                                                                                                                                                          ВP
                                                                                                                                                                     Myers
                                                                                                                                                                      EW
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              92;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                24;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Length
                                                                                                                                                                                                                                                                                                                         insecticide;
                                                                                                                                                                                                                                                                                                                                             8479.
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                                                                                                                   cell-cell
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useful in developmental biology and in elucidating cell signalling and insecticides, therapeutics and pharmaceutical development of discloses genomic DNA sequences (ABLIG176-ABL30511), expressed The sequences (ABLG177-ABB72072).

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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    16990
                                                                                                                                                                                                                                                                                                                           antirheumatic; antiarthritic; antidiabetic; antipsoriatic;
antiinflammatory; cancer; eye disease; arteriosclerosis; anaemia;
acute myeloid leukaemia; Alzheimer's disease; AIDS; epilepsy;
                                                                                                                                                                                                                                                                                                                                                                  Human; immune system disease; cytosine methylation; antiasthmatic; antiarteriosclerotic; antianaemic; cytostatic; nootropic; neuroprotective; anti-HIV; anticonvulsant; ophthalmological;
        Nucleic acid comprising fragment of chemically modified gene, useful for diagnosis and treatment of diseases associated with abnormal
                                                                                 Olek A,
                                                                                                                                                                                   02-JUL-2001; 2001WO-EP07537.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 \label{prop:specification} \begin{subarray}{ll} specification, but was obtained in electronic format directly at ftp.wipo.int/pub/published_pct\_sequences. \end{subarray}
                                                      WPI; 2002-130909/17.
                                                                                                                                        30-JUN-2000;
01-SEP-2000;
                                                                                                                                                                                                               03-JAN-2002.
                                                                                                                                                                                                                                           WO200200928-A2
                                                                                                                                                                                                                                                                      Homo sapiens.
                                                                                                                                                                                                                                                                                                  gene;
                                                                                                                                                                                                                                                                                                               neurofibromatosis;
                                                                                                                                                                                                                                                                                                                                                                                                                              Human
                                                                                                                                                                                                                                                                                                                                                                                                                                                          26-MAR-2002
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ABL32322 standard; DNA; 6418
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Sequence 21231 BP;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           GCCAGACCAAAAGTGTCCGTTTTACGAATCGAAAAAATTTTACGATTTTGAAAAAACGAAG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ATTAAACCTTAAATGGGCTTTCTATAAGGCCCCAATTATATTACGATTATAACAAAGTGAC
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             TTTTTTTTGCCCCAATGATATAAAAAATTTGGATAATAATATTATTGGATATTCGTTTT
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                                                                                                                                                                                                                                                                                                                                                                                                                             immune system associated
                                                                                                             EPIGENOMICS AG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Similarity
methylation
                                                                                 Piepenbrock
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Conservative
                                                                                                                                        2000DE-1032529
2000DE-1043826
                                                                                                                                                                                                                                                                                                                                                                                                                                                         (first entry)
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                                                                                                                                                                                                                                                                                                               rheumatoid arthritis;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           14.7%;
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                                                                                  Berlin
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ВP
                                                                                                                                                                                                                                                                                                                                                                                                                             gene SEQ ID NO:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Mismatches
                                                                                                                                                                                                                                                                                                              psoriasis;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                189;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      T; 0 other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Length 21231;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Indels
                                                                                                                                                                                                                                                                                                               epilepsy;
bowel dis
                                                                                                                                                                                                                                                                                                               disease;
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Search completed: March
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Best Local
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                                                                                                 1170
                                                                                                                                                        1110
                                                                                                                                                                                                                                                                                                            The present invention provides a number of human immune system associated genes which are modified by the methylation of cytosines. The sequences can be used in the diagnosis and treatment of immune system disorders, including eye diseases such as retinopathy, neovascular glaucoma and macular degeneration, arteriosclerosis, anaemia, cancer, acute myeloid leukaemia, Alzheimer's disease, AIDS, epilepsy, neurofibromatosis, rheumatoid arthritis, psoriasis and inflammatory/ulcerative bowel
                                                                                                                                                                                                                                                                     Sequence 6418 BP; 1842 A; 47 C; 1423 G; 3106 T; 0 other;
                                                                                                                                                                                                                                                                                              diseases. The present sequence is a gene of the invention.
                                                                                                                                                                                                                                                                                                                                                                                                                               Claim
                                                                     138
                                                                                                                                                                                  18
                                                                                                                             78
                                                                                                                                                                       TAATTGGATTTATTTTTGTTAGGGGATAATTTATTATGGTTTTTATTTA
                                                                    AAAGGGTTTCGACTTTCGAAAGTGGACGATGTATATAGATTGGGAGCTA
                                                                                              TATATAAAAATTTGGATAAATAATATTATTGGATATTCGTTTTTAGTTCGGGTTTGAGA 137
                                                                                                                                                                                                                                                                                                                                                                                                                               1;
                                                                                                                                                                                                                             Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                               SEQ
                                                                                                                                                                                                               Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                               IJ
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Pred. No. 0
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                                                                                                                                                                                                                                         DB
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                                                                                                                                                                                                               73;
                                                                                                                                                                                                                                                                                                                                                                                                                               German
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                                                                                                                                                                                                                                         Length
                                         1278
                                                                     186
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Perfect score:
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length: 2000000000
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1: /cgn2_6/ptodata/1,
2: /cgn2_6/ptodata/1,
3: /cgn2_6/ptodata/1,
4: /cgn2_6/ptodata/1,
5: /cgn2_6/ptodata/1,
6: /cgn2_6/ptodata/1,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                US-09-502-426A-1_COPY_6111_6468
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Match Length DB
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            March 29, 2003, 18:09:40; Search time 12.5196 Seconds (without alignments) 8769.450 Million cell updates/sec
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/cgn2_6/ptodata/1/ina/5B_COMB.seq:*
/cgn2_6/ptodata/1/ina/6A_COMB.seq:*
/cgn2_6/ptodata/1/ina/6B_COMB.seq:*
/cgn2_6/ptodata/1/ina/BCTUS_COMB.seq:*
/cgn2_6/ptodata/1/ina/backfiles1.seq:*
      1 US-08-340-820-24

US-08-593-535-24

US-09-122-400B-5

1 US-09-056-075-1

1 US-09-056-075-1

1 US-09-073-569-1

1 US-09-073-569-1

1 US-08-341-568-3

US-08-341-568-3

US-08-341-568-3

US-08-341-568-3

US-08-487-826B-13

US-08-487-826B-13

US-08-487-826B-13

US-08-487-826B-13

US-08-98-416-547

US-08-98-416-498

US-08-747-221B-24

US-08-747-221B-24

US-09-005-051-26

US-09-005-051-26

US-08-09-134-001C-2606

US-08-99-134-001C-2606
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10.4	10.4	10.4	10.4	10.4	10.4	10.5	10.5	10.5	10.5	10.5	10.6	10.6	10.6	10.6	10.6	10.6	10.6
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US-08-702-344-26	US-08-961-527-73	US-08-890-865A-2	US-09-817-180-1	5215909-9	US-08-887-534A-81	US-09-173-914-1	US-07-867-106-2	US-07-867-106-4	US-07-867-106-5	US-09-180-852-1	US-08-545-196B-12	US-08-545-196B-10	US-08-645-193B-18	US-08-466-961A-16	US-08-392-625-16	US-09-265-731-3	US-08-693-457-3
	Sequence 73, Appl	'n	Sequence 1, Appli	52	Sequence 81, Appl	Sequence 1, Appli	Sequence 2, Appli	Sequence 4, Appli	5	1, A	Sequence 12, Appl	•	Sequence 18, Appl	•	Sequence 16, Appl	Sequence 3, Appli	Sequence 3, Appli

ALIGNMENTS

## PILING DATE: CLASSIFICATION: 435 PRIOR APPLICATION DATA: APPLICATION NUMBER: US/07/835,713 APPLICATION NUMBER: US/07/835,713 . FILING DATE: ATTORNEY/AGENT INFORMATION: NAME: CONLIN, David G. REGISTRATION NUMBER: 27026 TELECOMMUNICATION INFORMATION: TELEPAN: (617)523-3400 TELEFAX: (617)523-440 TELEX: 200291 STRE UR TELEX: 200291 STRE UR INFORMATION FOR SEQ ID NO: 24: SEQUENCE CHARACTERISTICS: LENGTH: 1493 base pairs TYPE: DUCLEIC acid Sequence 24, Application US/08340820 Patent No. 5512460 GENERAL INFORMATION: MOLECULE TYPE: ( HYPOTHETICAL: NO ANTI-SENSE: NO COMPUTER READABLE FORM: MEDIUM TYPE: Floppy disk COMPUTER: IBM PC compatible OPERATING SYSTEM: PC-DOS/MS-DOS SOFTWARE: Patentin Release #1.0, Version #1.25 CURRENT APPLICATION DATA: APPLICANT: KONDO, Tatsuya TITLE OF INVENTION: GLIA ACTIVATING TITLE OF INVENTION: PRODUCTION NUMBER OF SEQUENCES: 27 CORRESPONDENCE ADDRESS: ORIGINAL SOURCE: ORGANISM: Hom APPLICANT: NARUO, Ken-ichi APPLICANT: SEKO, Chisako APPLICANT: KUROKAWA, Tsutomu APPLICANT: KONDO, Tatsuya TOPOLOGY: TYPE: nucleic acid STRANDEDNESS: double APPLICATION NUMBER: ADDRESSEE: ADDRESSEE: DAVID G. CONLIN; ADDRESSEE: CUSHMAN Massachusetts 130 Water Street linear Ö cDNA to mRNA US/08/340,820 DIKE, BRONSTEIN, ROBERTS FACTOR

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US-08-593-535-24/c
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                                                                                                       TELEFAX: (617)523-6440
TELEX: 200291 STRE UR
INFORMATION FOR SEQ ID NO:
                                                                                                                                                                                     PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 0:
FILING DATE: 12-FEB-1992
ATTORNEY/AGENT INFORMATION:
NAME: CONLIN, David G.
                                                                                                                                                                                                                                                                OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/593,535
FILING DATE: 24-JAN-1996
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      APPLICANT:
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           MOLECULE TYPE:
HYPOTHETICAL:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                      TITLE OF INVENTION: GLIA ACTIVATING FACTOR AND ITS TITLE OF INVENTION: PRODUCTION NUMBER OF SEQUENCES: 27 CORRESPONDENCE ADDRESS:
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LENGTH: 1493 base pairs
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TELEPHONE: (617)523-3400
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                                                                                                                                                                         NAME: CONLIN, David G. REGISTRATION NUMBER: 2
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                                        TOPOLOGY:
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KUROKAWA, Tsutomu
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IBM PC compatible
SYSTEM: PC-DOS/MS-DOS
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; ORGANISM: Nicotiana tabacum
US-09-122-400B-5
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US-08-593-535-24
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SEQ ID NO 5
LENGTH: 998
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Patent No. 6245974
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Best Local Similarity
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Best Local :
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                                                                                                                                                                                                                                                                                                                                                                                                       APPLICANT: Spiker, Steven
TITLE OF INVENTION: MATRIX ATTACHMENT REGIONS
                                                                                                                                                                                                                                                                                                                                          PRIOR APPLICATION NUMBER: 60/
PRIOR FILING DATE: 1997-08-06
                                                                                                                                                                                                                                                                                                                                                                                                                     APPLICANT: Michalowski, Susan APPLICANT: Spiker, Steven
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IMMEDIATE SOURCE:
LIBRARY: Human
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439 TCAGCTTCTTTTTTTCAGTTTTTA 415
                      185 TAGGTTGAGTCTTTGGACATTTGTA 209
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                                                            125 TTCGGGTTTGAGAAAAGGGTTTCGACTTTCGAAAGTGGACGATGTATATAGATTGGGAGC 184
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                                                                                                                                                                        TATAAAAATTTGGATAAATAATATTATTGGATATTCGTTTTTAGTTCGGGTTTGAGAAA 139
                                               TTTTGCCCCAATGATATAAAAATTTTGGATAATAATATTATTGGATATTCGTTTTTTAG 124
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Pred. No. 1
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US-08-378-313-24/c ; Sequence 24, Application US/08378313 ; Patent No. 6207881

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US-08-378-313-24
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INFORMATION FOR SEQ ID NO:
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APPLICANT: THEOLO
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MEDIUM TYPE: Floppy disk
1922
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                                                         1982
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ATTORNEY/AGENT INFORMATION:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    TITLE OF INVENTION: CONTROL OF FRUIT RIPENING THROUGH
                                                                                                                                             184
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STRANDEDNESS: sing
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            APPLICATION NUMBER: US 0 FILING DATE: 02-APR-1992
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       FILING DATE:
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TTTGCATTCATTAATTAGCTAAGACAAATTATGATGTCTAAGTAC 1878
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                                                                                                                                                                                                                                TTTTACTTCGTTTTTGATCCGAAGCAATAACAAATTGTCAAATAC 348
                                                        AAACCTTAAAATGGGCTTTCTATAAGGCCCAATTATATTACGATTATAACAAAGTGACAAC 303
                                                                                                                CTAGGTTGAGTCTTTGGACATTTGTATTGGATGTTGTTGATTAGTGTCGACACTATT 243
                                                                                                                                                                        TTAACATAACTTCACTTTTGCATTCATTAATTAGCTAAGACAAATTATGATGTCTAAGTA 2043
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Similarity 44.9%;
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Patent No. 5955368
                                                                                                                                                                                                                                                                                                                                        Query Match
Best Local
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INFORMATION FOR SEQ ID NO:
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TELECOMMUNICATION INFORMATION:
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ATTORNEY/AGENT INFORMATION:
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MEDIUM TYPE: Floppy disk
                                                                                                                                                                                                       1356
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      SOFTWARE: Patentin Release #1.0, Version #1.30 CURRENT APPLICATION DATA:
                                                                                                                                               1296
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                            NUMBER OF SEQUENCES:
                                                                                                                                                                       123 AGTTCGGGTTTGAGAAAAGGGTTTCGACTTTCGAAAGTGGACGATGTATATAGATTGGGA 182
303
                                                        243 TAAACCTTAAATGGGCTTTCTATAAGGCCCAATTATATTACGATTATAACAAAGTGACAA 302
                                                                                                                                                                                                                                  64
                                                                                                                                                                                                                                                                                                                                                                                              OTHER INFORMATION: /note- "RP4 origin of DNA transfer (oriT) from OTHER INFORMATION: plasmid RP4"
                                                                                                                                                                                                                                                                                                                                     Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                         NAME/KEY: misc_feature LOCATION: 3770..4013
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   COMPUTER: IBM PC compatible OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     STREET:
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CTTTTACTTCGTTTTTGATCCGAAGCAA 330
                                                                                                                  GCTAGGTTGAGTCTTTGGACATTTGTATTGGATGTTGTTTGATTATTAGTGTCGACACTAT
                                                                                                                                                                                                                                 TTTTTGCCCAATGATATAAAAATTTGGATA-AATAATATTATTGGATATTCGTTTTTT 122
                                                                                                                                            Madison
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               6243 base pairs
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1 South Pinckney S:
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Bradshaw, Marite
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47.3%;
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Pred. No. 2
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                                                                                                            Query Match
Best Local :
                                                                                                Matches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                           SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 TELEPHONE: (215) 962-4130
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        APPLICATION NUMBER: PC
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                                                                                                                                                                                                                                                                                                                                                                                                         MOLECULE TYPE:
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APPLICANT: Shani, Moshe
TITLE OF INVENTION: Transgenic Protein Production
NUMBER OF SEQUENCES: 1
                                                                                                                                                                                                                                                                                                                                                                  PUBLICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                  ANTI-SENSE:
                                                                                                                                                                                                                                                                                                                                                                                             HYPOTHETICAL:
                                        COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Polocial
                62
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           NAME: Goodman, Rosanne REGISTRATION NUMBER: 52, REFERENCE/DOCKET NUMBER:
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                                                                                                           Local Similarity
                                                                                                                                                               RELEVANT RESIDUES IN SEQ ID
                                                                                                                                                                                                                                                                          AUTHORS:
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                                                     AUTHORS:
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TTTTTTTGCCCAATGATATAAAAAATTTGGATAAATAATAATATTATTGGATATTCGTTTTT 121
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MOLECULAR STRUCTURE OF THE HUMAN ALBUMIN GENE
IS REVEALED BY NUCLEOTIDE SEQUENCE WITHIN Q11-22
OF CHROMOSOME 4
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261
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Dennison, O E
Hawkins, J W
Beattie, W G
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                                                                                                                                                                                                                                                                                                                                         Minghetti, P P Ruffner, D E
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                                                                                              Conservative
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Pred. No. 2.3;
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Best Local S
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1595
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                                                                                                                                                                                                                                                       FEATURE:
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                                                                                                                                                                                                                                                                                                                                                                                                                       ATTORNEY/AGENT INFORMATION: NAME: Sawislak, Deborah
                                                                                                                                                                                                                                                                                                                                                                                                                                                            PRIOR APPLICATION DATA: APPLICATION NUMBER:
                       140
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CORRESPONDENCE ADDRESS:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 NAME/KEY:
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                                                                                                                        OPERATING SYSTEM:
SOFTWARE: FastSEC
                                                                                                                                                                                                                  OTHER INFORMATION:
                                                                                                                                                                                                                                                                   TOPOLOGY:
                                                                                                                                                                                                                                                                                STRANDEDNESS:
                                                                                                                                                                                                                                                                                                                                                         TELEFAX: 206-442-6678
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                                                                                                                                                                                                                                                                                                                                                                                                                                                 FILING DATE:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 APPLICATION NUMBER: FILING DATE:
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                       AGGGTTTCGACTTTC 154
                                                                       TATAAAAATTTGGATAAATATTATTGGATATTCGTTTTTTAGTTCGGGTTTGAGAAA 139
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                                               Similarity
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1201 Eastlake Avenue East
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                                                                                                                                                                                                                            Coding Sequence 34...1344
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Pred. No. 2.
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APPLICANT: DZIBGIEL, MORTEN;BORRE, MARTIN;JEPSEN, SOREN;
VUUST, JENS;RIENECK, KLAUS;WIND, ANNETTE;JAKOBSEN, PALLE H.
TITLE OF INVENTION: MALARIA ANTIGEN
NUMBER OF SEQUENCES: 19
CURRENT APPLICATION DATA:
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Best Local Similarity
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                                    REGISTRATION NUMBER: 28,005
REFERENCE/DOCKET NUMBER: BEI
TELECOMMUNICATION INFORMATION:
TELEPHONE: (202)628-5197
TELEPAX: (202)737-3528
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                         CURRENT APPLICATION DATA
                                                                                                                     ATTORNEY/AGENT INFORMATION:
                                                                                                                                                          PRIOR APPLICATION DATA:
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APPLICATION NUMBER: WO POSITION DATE: 19-AUG-1992
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ITTLE OF INVENTION: HUMAN BETA-CASEIN PROCESS FOR PRODUCING
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    APPLICANT:
                                                                                           NAME: COOPER, IVER P. REGISTRATION NUMBER: :
                                                                                                                                       APPLICATION NUMBER: FILING DATE: 19-AU
                                                                                                                                                                                                                                  APPLICATION NUMBER: U
                                                                                                                                                                                                                       CLASSIFICATION:
                                                                                                                                                                                                                                                                               SOFTWARE:
                                                                                                                                                                                                                                                                                                       COMPUTER:
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                                                                                                                                                                                                                                                                                                                   MEDIUM TYPE:
                                                                                                                                                                                                                                                                                                                                                            COUNTRY:
                                                                                                                                                                                                                                                                                                                                                                                        CITY: WASHINGTON
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                                                                                                                                                                                                                                                                                                                                                                                                419 SEVENTH STREET, N.W.
                                                                                                                                                                                                                                                                                                                                                             USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            HERNELL, OLLE
LOENNERDAL, BO
HJALMARSSON, KAI
                                                                                                                                                                                                                                                                      PatentIn Release #1.0, Version #1.25
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SYSTEM: PC-DOS/MS-DOS
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                                                                                                                                 19-AUG-1991
                                                                                                                                                                                                                                                                                                                 Floppy disk
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Pred. No. 2.5;
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RESULT 10
US-08-749-522-2
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                 Query Match
Best Local Similarity
          Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Patent No. 6096950
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Query Match
                                                                                                                                             INFORMATION FOR SEQ ID NO:
                                                                                                                                                                                          ATTORNEY/AGENT INFORMATION:
NAME: Baket, Jean C.
REGISTRATION NUMBER: 35,433
REFERENCE/DOCKET NUMBER: 670
                                                                                                                                                                                                                                                                                                      COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                 SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                             SOFTWARE: PatentIn Release #1.0, Version #1.25 CURRENT APPLICATION DATA:
                                                                      MOLECULE TYPE:
                                                                                                                                                                     TELEPHONE: (414) 277-5709
                                                                                                                                                                                                                                                                                                                                                                                                                                    CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                           TITLE OF INVENTION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          1043 GTAGATTAGT 1052
                                                                                                                                                                                                                                                                                                                                                                                                                                                  NUMBER OF SEQUENCES:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                FEATURE:
                                                                                STRANDEDNESS:
TOPOLOGY: 11
                                                                                                 TYPE: nucleic acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           MOLECULE TYPE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 180 GGAGCTAGGT 189
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  120 TTTAGTTCGGGTTTGAGAAAAGGGTTTCGACTTTCGAAAGTGGACGATGTATATAGATTG 179
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   923 ATTTATAGTATAGAAATGAGTATAAAAACTAGTATAATTAGTATTAGTATATATTAGTAT 982
                                                                                                                                                                                                                                            FILING DATE:
CLASSIFICATION: 800
                                                                                                                                                                                                                                                                  APPLICATION NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                                CITY: Milwaukee
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           COUNTRY:
                                                                                                                                                                                                                                                                                                                                                                                                             STREET:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    INFORMATION:
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53202-4497
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Application US/08749522
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       Conservative
                                                                                                                                                         (414)
                                                                                 linear
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..6886, 7991..8521, 9440..9445)
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                                                                  DNA (genomic)
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                  11.2%;
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56.9%;
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  Score 40; DB 3; Le
Pred. No. 3.3;
0; Mismatches 180;
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Pred. No. 2.
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US-08-341-568-3/c
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                                                                                                                                                        TELEX: 248345
INFORMATION FOR SEQ ID NO:
                                                                                                                                                                                                            ATTORNEY/AGENT INFORMATION:
NAME: MULPHY Jr, Gerald M
REGISTRATION NUMBER: 28,977
REFERENCE/DOCKET NUMBER: 365-262P
TELECOMMUNICATION INFORMATION:
TELEPHONE: (703) 205-8000
                                                                                                                                                                                                                                                                                                                                             SOFTWARE: PatentIn Release #1.0, V
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/341,568
FILING DATE: 22-NOV-1994
                                                                                                                                                                                                                                                                                                                                                                                                                                                                 COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            APPLICANT: Saloheimo, Anua APPLICANT: Marjatta, Ranua TITLE OF INVENTION: Mannana TITLE OF INVENTION: methods TITLE OF INVENTION: pulps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              2344
                    MOLECULE TYPE:
ORIGINAL SOURCE:
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                                                                                                                                      SEQUENCE CHARACTERISTICS:
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CORRESPONDENCE ADDRESS:
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                                                                                                                                                                          TELEPHONE: (703) 205-8050
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ADDRESSEE: Birch, Stewart, Kolasch and Birch
STREET: PO Box 747
CITY: Falls Church
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           66
                                                                                          LENGTH: 289 base pairs
                                                                                                                                                                                                                                                                                                                                                                                                                             COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          COUNTRY: US
ZIP: 22040-0747
ORGANISM:
                                                              TOPOLOGY:
                                                                            STRANDEDNESS:
                                                                                                                                                                                                                                                                                                                                   CLASSIFICATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    TAGGTTGAGTCTTTGGACATTTGTATTGGATGTTGTTGATTATTAGTGTCGACACTATTA 244
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Penttila, Merja
                                                                                                                                                                                                                                                                                                                                                                                                           PatentIn Release #1.0, Version #1.30
  Trichoderma
                                                          linear
                                        CDNA
                                                                          single
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Best Local :
               Query Match
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                                                                                                                                                                                             TELEX: 248345
INFORMATION FOR SEQ ID NO:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               GENERAL INFORMATION:
                                                          MOLECULE TYPE: cDI
ORIGINAL SOURCE:
ORGANISM: Trichd
STRAIN: QM9414
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               APPLICANT:
                                                                                                                                                                                                                                     REFERENCE/DOCKET NUMBER: 36
TELECOMMUNICATION INFORMATION:
TELEPHONE: (703) 205-8000
                                                                                                                                                                                                                                                                                                           APPLICATION NUMBER: US 0
FILING DATE: 22-NOV-1994
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                        CLASSIFICATION: 435
PRIOR APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                              COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                           COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
                                                                                                                                                                             SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           TITLE OF INVENTION: Mannanase enzymes, genes coding for them, TITLE OF INVENTION: methods for isolating the genes, and meth TITLE OF INVENTION: lignocellulosic pulps
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                                                                                                                                                                                                                                                                                                                                                                                     APPLICATION NUMBER: FILING DATE: 13-AU
                                                                                                                      TOPOLOGY:
                                                                                                                                  STRANDEDNESS:
                                                                                                                                                                                                                          TELEFAX:
                                                                                                                                                                                                                                                                                NAME: Murphy Jr, Gerald M
REGISTRATION NUMBER: 28,977
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                                                                                                                                                               LENGTH: 289 base pairs
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                                                                                                                                                  nucleic acid
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PO Box 747
                                                                                                                                                                                                                        (703) 205-8050
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Marjatta, Ranua
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Viikari, Liisa
Penttila, Merja
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                                                                         Trichoderma reesei
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Score 39.4; D
Pred. No. 4.3;
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Pred. No. 4.3;
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            Length 289;
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Matches

Conservative

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Mismatches

Indels

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Gaps

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Best Local Similarity

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; MOLECULE TYPE:
; HYPOTHETICAL: N
; ANTI-SENSE: NO
US-08-487-826B-13
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US-08-487-826B-13/c
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15755
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INFORMATION FOR SEQ ID NO:
                       126 TCGGGTTTGAGAAAAGGGTTTCGACTTTCGAAAGTGGACGATGTATATA---GATTGGGA 182
                                                                                                                                                                                                                                                                                                     SEQUENCE CHARACTERISTICS:
LENGTH: 19124 base pai
                                                                                                                                                                                                                                                                                                                                                                                                                        COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/487,826B
FILING DATE: 10-SEP-1993
CLASSIFICATION: 435
CLASSIFICATION: 435
                                                                                                                                                                                                                                                                                                                                                                   REFERENCE/DOCKET NUMBER: NI
TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                             ATTORNEY/AGENT INFORMATION:
NAME: Israelsen, Ned
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      tent No.
                                                                 66 TTTGCCCAATGATAATAAAAATTTGGATAAATAATAATATTGGATATTCGTTTTTTAGT 125
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          NUMBER OF SEQUENCES: 4
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  TITLE OF INVENTION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              APPLICANT: Sim, Kim L.
APPLICANT: Chitnis, Chetan
APPLICANT: Miller, Louis H.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             APPLICANT:
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                                                                                                                 Local Similarity
                                                                                                                                                                                                                                                                    TOPOLOGY:
                                                                                                                                                                                                                                                                         STRANDEDNESS:
                                                                                                                                                                                                                                                                                                                                                       TELEPHONE:
                                                                                                                                                                                                                                                                                                                                                                                        NAME: Israelsen, Ned REGISTRATION NUMBER: 29,655
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     STREET: 620 Newport Center Drive CITY: Newport Beach STATE: California
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             217 TATATATATTCATCAAAAA 197
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     277
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5. 5993827
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                                                                                                                                                                                                                                                                                          H: 19124 base pairs nucleic acid
                                                                                                                                                           Conservative
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                                                                                                                                                                                                                                                              linear
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0 Newport Center Drive 16th Floor
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AND PLASMODIUM FALCIPARUM ERYTHROCYTE BINDING PROTEINS
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Pred. No. 4
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; TYPE: DNA
; ORGANISM: Populus balsamifera subsp. trichocarpa
;US-09-410-464-1
Query Match
Best Local Similarity
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; TYPE: DNA
; ORGANISM: Brachydanio rerio (zebra fish)
US-09-444-336-7
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                                                                                                                                       SOFTWARE:
SEQ ID NO 1
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Patent No. 6395892
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                                                                                                                                                                                                     CURRENT APPLICATION NUMBER: US/09/410,464
CURRENT FILING DATE: 1999-10-01
EARLIER APPLICATION NUMBER: 09/287,700
EARLIER FILING DATE: 1999-04-06
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Query Match
Best Local Similarity
                                                                                                                                                                         EARLIER APPLICATION NUMBER: 60/080,851 EARLIER FILING DATE: 1998-04-06
                                                                                                                                                                                                                                                     APPLICANT: Strauss et al.
TITLE OF INVENTION: Floral homeotic genes for manipulation of flowering in
TITLE OF INVENTION: poplar and other plant species.
FILE REFERENCE: 53375
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  SOFTWARE: PatentIn Ver. 2.1 SEQ ID NO 7
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Sequence 7, Application US/09444336 Patent No. 6410713 GENERAL INFORMATION:
                                                                                                                                                               NUMBER OF SEQ ID NOS: 24
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 APPLICANT: Guerriero, Vincent
APPLICANT: Raynes, Deborah A
TITLE OF INVENTION: DNA Encoding Proteins That Inhibit Hsp70 Function
FILE REFERENCE: HspBr DNA and Protein Sequences
CURRENT APPLICATION NUMBER: US/09/444,336
CURRENT FILING DATE: 1999-11-19
EARLIER APPLICATION NUMBER: 60/109,351
EARLIER FILING DATE: 1998-11-20
                                                                                                                       LENGTH: 4285
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         1802 GGTCTGAATGTGTTTAATTTAATTATTGTCTATT 1768
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      80 TATAAAAATTTGGATAAATAATATTATTGGATATT 114
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              303 CTTTTACTTCGTTTTTGATCCGAAGCAATAACAAATTGTCAAATA 347
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              Conservative
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                         10.9%;
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        Score 39; DB Pred. No. 5.2; 0; Mismatches
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Pred. No. 5.2;
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                        DB 4; Length 4285;
5.2;
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Listing first 45 summaries
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Perfect score:
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Gapop 10.0 , Gapext 1.0
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358
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              GenCore version 5.1.4_p5_4578 Copyright (c) 1993 - 2003 Compugen Ltd.
                                                                                                                                                                                                                                                                                                                                                                                                                                                  /cgn2_6/ptodata/1/pubpna/US06_PUBCOMB.seq:*
/cgn2_6/ptodata/1/pubpna/US07_NEW_PUB.seq:*
/cgn2_6/ptodata/1/pubpna/PCTUS_PUBCOMB.seq:*
/cgn2_6/ptodata/1/pubpna/US08_NEW_PUB.seq:*
/cgn2_6/ptodata/1/pubpna/US08_NEW_PUB.seq:*
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                                                                                                                                                                                                                                                                                   Length
               2003, 08:25:26; Search time 27.2667 Seconds (without alignments) 11172.915 Million cell updates/sec
 US-10-102-800-9-12673
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) US-09-960-352-5094
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US-10-102-806-401
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Sequence 5785, Apsequence 401, App Sequence 12673, A Sequence 26, Appl Sequence 360, Appl Sequence 340, App Sequence 3759, App Sequence 3759, App Sequence 345, App
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US-09-960-352-5785
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Best Local
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US-09-960-352-1243	US-09-885-2032-11	[[S-09-960-353-4584	US-09-813-153-35	US-09-816-894-5	US-09-960-353-1707	US-09-880-107-706	US-10-013 433 6	TIS-00-005 300 31-	TIS=00+734-674-3	IIS-10-374-990-3	IIS-09-950-353-8556	TS-00-878-574 13633	IIS-09-939-8428 4265	TS-00-060-3E2 124:5	TS-09-754-9531-3	US-09-754-9533-3	US-09-880-107-3337	C#C-141 / 121 Of C#C	US-10-141-755-345	IIS-10-131-050-345	US-10-142-423-345	US-10-123-262-245	US-10-142-419-345	US-10-140-002-245	US-10-143-114-345
Sequence 11, Appl Sequence 1243, Ap	Sequence 4584, Ap	Sequence 35, Appl	Sequence 5, Appli	Sequence 1707, Ap	Sequence 706, App	Sequence 2, Appli	Sequence 315, App	Sequence 3, Appli	Sequence 3, Appli	Sequence 5558, Ap	Sequence 13973, A	Sequence 4296, Ap	Sequence 12412, A	Sequence 3, Appli	Sequence 2, Appli	Sequence 3327, Ap	Sequence 20, Appl	Sequence 345, App	Sequence 345, App	Sequence 345, App	sequence 345, App	Sequence 345, App		Sequence 345, App	

## ALIGNMENTS

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RESULT 2
US-10-102-806-401/c
; Sequence 401, Application US/10102806
                                                                                                                                                                                                                                                                                                                                                                      APPLICANT: Warren, Wesley C.
APPLICANT: Tao, Nengbing
APPLICANT: Tao, Nengbing
APPLICANT: Tao, Nengbing
APPLICANT: Mathalagan, Nagappan
TITLE OF INVENTION: NUCLEIC ACID AND OTHER MOLECULES ASSOCIATED WITH LACTATION AND
FILE REPERENCE: 16511.006/37-21(10298)C
CURRENT APPLICATION NUMBER: US/09/960,352
NUMBER OF SEQ ID NOS: 15112
SEQ ID NO 5785
LENGTH: 516
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                sequence 5785, Application US/09960352
Patent No. US20020137139A1
                                                                                                                                                                                                                                                                      FEATURE:
NAME/KEY: unsure
LOCATION: (76), (90)
OTHER INFORMATION: unsure at all n locations
OTHER INFORMATION: Clone ID: 25-LIB3057-018-Q1-K1-G1
                                                                                                                                                                                                                                                                                                                                                            TYPE: DNA
ORGANISM: Bos taurus
                                                                                                                                80 TATAAAAATTTGGATAAATAATATTATTGGATATTCGTTTTTTAGTT 126
                                                                                                                                                   Similarity 65.470; Conservative
                                                                                                                                                                                                                      13.4%;
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Publication No.

US20030054421A1

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US-09-960-352-12673/c
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                                                                    SEQ ID NO 12673
LENGTH: 277
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SEQ ID NO 401
LENGTH: 189
TYPE: DNA
                                                                                                  APPLICANT: Tao, Nengbing
APPLICANT: Byatt, John C.
APPLICANT: Byatt, John C.
APPLICANT: Byatt, John C.
APPLICANT: Mathialagan, Nagappan
TITLE OF INVENTION: NUCLEIC ACID AND OTHER MOLECULES ASSOCIATED WITH LACTATION AND
FILE OF INVENTION: MUSCLE AND FAT DEPOSITION
FILE REFERENCE: 15511.006/37-21(10298)C
CURRENT APPLICATION NUMBER: US/09/960,352
CURRENT FILING DATE: 2001-09-24
NUMBER OF SEQ ID NOS: 15112
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CURRENT FILING DATE: 2002-03-22
PRIOR APPLICATION NUMBER: 09/925,298
PRIOR FILING DATE: 2001-08-10
PRIOR APPLICATION NUMBER: PCT/US00/05881
PRIOR FILING DATE: 2000-03-08
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                                                                                                                                                                                                                                                                     APPLICANT: Warren, Wesley C.
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TITLE OF INVENTION: Nucleic Acids, Proteins and Antibodies
FILE REFERENCE: PA103PLC1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    PRIOR APPLICATION NUMBER: 60/124,270 PRIOR FILING DATE: 1999-03-12
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                NUMBER OF SEQ ID NOS: 846
                                                    TYPE: DNA
                OTHER INFORMATION:
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OTHER INFORMATION: n equals a,t,g,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 LOCATION: (162)
OTHER INFORMATION: n equals
NAME/KEY: misc_feature
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     NAME/KEY: misc_feature
LOCATION: (187)
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LOCATION: (166)
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LOCATION: (162)
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OTHER INFORMATION: n equals
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        NAME/KEY: misc_feature LOCATION: (1)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     98 TATTAAAATAAACATGTATAGCAGGTTTCAACAATTGTCTTGTAGTTTG 50
                                                                                                                                                                                                                                                                                                                                                                                                                                                      80
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                  TATAAAAATTTGGATAAATAATATTATTGGATATTCGTTTTTTAGTTCG 128
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                INFORMATION: n equals a,t,g, or
Bos taurus
ORMATION: Clone ID: 54-LIB3058-039-Q1-K1-F10
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Pred. No.
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                                            APPLICANT: Warren, Wesley C. APPLICANT: Tao, Nengbing
              APPLICANT:
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US-09-960-352-5094
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Sequence 5094, Application US/09960352 Patent No. US20020137139A1 GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                     Matches
                                                                                                                                                                                                                                                                                                                                                                                                     SOFTWARE: PatentIn Ver. SEQ ID NO 26
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APPLICANT: Genetics Institute, Inc.
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Best Local Similarity 57.6%;
Matches 80; Conservative
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                                                                                                                                                                                                                                                                                                                 Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                      PRIOR APPLICATION NUMBER: 60/195,604
PRIOR FILING DATE: 2000-04-06
NUMBER OF SPORTS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                              FILE REFERENCE: GIN 6402
CURRENT APPLICATION NUMBER: US/09/822,830A
CURRENT FILING DATE: 2001-03-29
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           APPLICANT: Graham, James R.
TITLE OF INVENTION: POLYNUCLEOTIDES ENCODING NOVEL SECRETED PROTEINS
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TYPE: DNA
ORGANISM: Homo sapiens
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                                                                                                        441
                                                                                                                                   140
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                                                                                                                                                                                                                                                     62 TTTTTTTGCCCCAATGATATATAAAATTTGGATAAATATATTATTTGGATATTCGTTTTT
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                                                                                                                                  AGGGTTTCGACTTTCGAAAGTGGACGATGTATATAGATTGGGAGCTAGGTTGAGTCTTT 198
                                                                                                                                                               TATAAAAATTTGGATAAATAATATTATTGGATATTCGTTTTTTAGTTCGGGTTTGAGAAA 139
                                                                                                                                                                                                                         95;
                                                                                                                                                                                                                                                                                                   Similarity
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S20020142952A1
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Howes, Steven H.
Resnick, Richard J.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Gulukota, Kamalakar
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                                                                                                                                                                                                                                                                                                  12.5%;
53.1%;
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Māthialagan, Byatt,

CURRENT APPLICATION NUMBER: US/09/960,352 CURRENT FILING DATE: 2001-09-24

TITLE OF INVENTION: NUCLEIC ACID AND OTHER MOLECULES ASSOCIATED WITH LACTATION AND TITLE OF INVENTION: MUSCLE AND FAT DEPOSITION FILE REFERENCE: 16511.006/37-21(10298)C

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                                                                                                                                                                                              Matches 114; Conservative
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Best Local Similarity
                                                                                                                                                                                                                                                                                                                       APPLICANT: Warren, Wesley C.
APPLICANT: Tao, Nengbing
APPLICANT: Tao, Nengbing
APPLICANT: Byatt, John C.
APPLICANT: Mathalagan, Nagappan
TITLE OF INVENTION: NUCLEIC ACID AND OTHER MOLECULES ASSOCIATED WITH LACTATION AND
TITLE OF INVENTION: MUSCLE AND FAT DEPOSITION
FILE REFERENCE: 16511.006/37-21(10298)C
CURRENT APPLICATION NUMBER: US/09/960,352
CURRENT FILING DATE: 2001-09-24
                                                                                                                                                                                                                                                                                                                                                                                                                                                           GENERAL INFORMATION:
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SEQ ID NO 5094
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TYPE: DNA
ORGANISM: Bos taurus
FEATURE:
      200 GACATTTGTATTGGATGTTGTTGATTATTAGTGTCGACACTATTAAACCTT 250
                                                                                                203
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LOCATION: (17),(37),(41)
OTHER INFORMATION: unsure at all n locations
OTHER INFORMATION: Clone ID: 22-LIB3058-042-Q1-K1-F9
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                                                                                 TATAAAAATTTGGATAAATAATATTATTGGATATTCGTTTTTTAGTTCGGGTTTGAGAAA 139
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                                                                                                                                                                                                          12.28;
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                                                                                                                                                                                            0; Mismatches
                                                                                                                                                                                                       Score 43.8; D
Pred. No. 4.6;
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Pred. No. 4;
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                                                                                                                                                                                                                                                                                                                                                                                                ; LENGTH: 447
; TYPE: DNA
; ORGANISM: Arabidopsis thaliana
US-09-770-444-759
                                                                                                                                                    GENERAL INFORMATION:
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                                                                                                                                                                                                                                                                                                                                                                Query Match
Best Local ;
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LENGTH: 413
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TITLE OF INVENTION: Expressed Sequences of Arabidopsis
TITLE OF INVENTION: thaliana
FILE REFERENCE: 2027 (PARA-016PRV)
CURRENT APPLICATION NUMBER: US/09/770,444
CURRENT FILING DATE: 2001-01-26
PRIOR APPLICATION NUMBER: 60/178,502
PRIOR APPLICATION NUMBER: 60/178,502
PRIOR FILING DATE: 2000-01-27
NUMBER OF TILING DATE: 2000-01-27
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APPLICANT:
APPLICANT:
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                                                                                                                                                                                                                                                                                                                                                             Local
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57; Conserv
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Hamilton, Carol M
Price, Jennifer L
Raines, Tracy M.
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Woessner, Jeffrey P.
Haas, William David
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Rameaka, Joshua G.
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Pred. No. 4.
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APPLICANT: Warren, Wesley C.
APPLICANT: Tao, Nengbing
APPLICANT: Byatt, John C.
APPLICANT: Byatt, John C.
APPLICANT: Mathialagan, Nagappan
TITLE OF INVENTION: NUCLEIC ACID AND OTHER MOLECULES ASSOCIATED WITH LACTATION AND
TITLE OF INVENTION: MUSCLE AND FAT DEPOSITION
TITLE OF INVENTION: MUSCLE AND FAT DEPOSITION
CURRENT ELIVERATION NUMBER: US/09/960,352
CURRENT APPLICATION NUMBER: US/09/960,352
NUMBER OF SEQ ID NOS: 15112
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US-09-770-444-759
                                                                                                                                                                                                                                                                                                                                                                                                                                Length 447;
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RESULT 10
US-10-028-072-345/c
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; Publication No. US;
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; TYPE: DNA
; ORGANISM: Bos taurus
; OTHER INFORMATION: Clone
US-09-960-352-6528
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Best Local Similarity
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APPLICANT: Tao, Nengbing
APPLICANT: Byatt, John C.
APPLICANT: Byatt, John C.
APPLICANT: Mathialagan, Nagappan
TITLE OF INVENTION: NUCLEIC ACID AND OTHER MOLECULES
TITLE OF INVENTION: MUSCLE AND FAT DEPOSITION
FILE REFERENCE: 16511.006/37-21(10298)C
CURRENT APPLICATION NUMBER: US/09/960,352
CURRENT FILING DATE: 2001-09-24
NUMBER OF SEO ID NOS: 15112
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ORMATION: Clone ID: 13-LIB3058-032-Q1-K1-D1
  Application US/10028072
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Pred. No. 4
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FILLING DATE: 1997-10-28
APPLICATION NUMBER: 60/063704
FILLING DATE: 1997-10-29
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FILING DATE: 1997-10-27
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APPLICATION NUMBER: 60/062816
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Watanabe, Colin
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Godowski, Paul J.
Gurney, Austin L.
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FILING DATE: 1998-05-07
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APPLICATION NUMBER: 60/069694
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APPLICATION NUMBER: 60/069212
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APPLICATION NUMBER: 60/066453
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JR FILING DATE: 1998-06-04
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JR APPLICATION NUMBER: 60/088741
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FILING DATE: 1998-07-01
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APPLICATION NUMBER: 60/090538
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APPLICATION NUMBER:
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FILING DATE: 1998-06-19
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APPLICATION NOTE: 1998-06-17
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FILING DATE: 19/98-06-11
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APPLICATION NUMBER: 60/
FILING DATE: 1998-06-10
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63.5%;
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5-13
                                            Score 43.2; D
Pred. No. 10;
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APPLICANT:

Deforge, Laura Desnoyers, Luc Filvaroff, Ellen

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; SEQ ID NO 345
; LENCTH: 2933
; TYPE: DNA
; ORGANISM: Homo Sapien
US-10-121-049-345
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US-10-123-904-345/c
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               Prior Application removed - See File Wrapper or Palm
NUMBER OF SEQ ID NOS: 550
SEQ ID NO 345
LENGTH: 2933
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GENERAL INFORMATION
                                                                                                                                                                                                                                                                                                                                                                                                                                                           Sequence 345, Application US/10123904 Publication No. US20030022328A1
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                                                                             CURRENT APPLICATION NUMBER: US/10/123,904 CURRENT FILING DATE: 2002-04-16
                                                                                                            APPLICANT: Zhang, Zemin
TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC
TITLE OF INVENTION: ACIDS ENCODING THE SAME
FILE REFERENCE: P3330R1C54
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CURRENT FILING DATE: 2002-04-12
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TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC
TITLE OF INVENTION: ACIDS ENCODING THE SAME
FILE REFERENCE: P3330R1C17
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TYPE: DNA
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Goddard, Audrey
Godowski, Paul J.
Gurney, Austin L.
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Watanabe, Colin K
Wood, William
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Godowski, Paul J.
Gurney, Austin L.
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Pred. No. 10;
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US-10-140-470-345
                                                                                                                RESULT 14
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                                                      Sequence 345, Application US/10175746 Publication No. US20030027270A1 GENERAL INFORMATION:
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Best Local :
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Best Local :
APPLICANT:
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CURRENT APPLICATION NUMBER: US/10/140,470

CURRENT FILING DATE: 2002-05-06
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                                          Baker, Kevin P.
          Beresini, Maureen
DeForge, Laura
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Wood, William
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Pred. No. 10;
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Pred. No. 1
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APPLICANT:

Filvaroff,Ellen

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; APPLICANT: Zhang, Zemin
; TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC
; TITLE OF INVENTION: ACIDS ENCODING THE SAME
; CURRENT APPLICATION NUMBER: US/10/176,918
; CURRENT APPLICATION NUMBER: US/10/176,918
; CURRENT FILING DATE: 2002-06-20
    Prior Application removed - See File Wrapper or Palm
; NUMBER OF SEQ ID NOS: 550
; LENGTH: 2933
; TYPE: DNA
ORGANISM: Homo Sapien
US-10-176-918-345
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US-10-176-918-345/c
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Best Local Similarity 63.5%;
Matches 66; Conservative
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CURRENT APPLICATION NUMBER: US/10/175,746
CURRENT FILING DATE: 2002-06-19
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Watanabe, Colin K
Wood, William
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Gurney, Austin L.
Sherwood, Steven
Smith, Victoria
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Godowski, Paul J.
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## ALIGNMENTS

JOURNAL REFERENCE AUTHORS TITLE JOURNAL REFERENCE AUTHORS TITLE REFERENCE AUTHORS SOURCE ORGANISM VERSION KEYWORDS RESULT 1 AL762543 LOCUS ACCESSION DEFINITION TITLE Li,Y., Strizhov,N., Rosso,M. and Weisshaar,B. Direct Submission Submitted (17-JUN-2002) Weisshaar B., Max-Pla Strizhov,N., Li,Y., Rosso,M., Viehoever,P., Dekker,K., Saedler,H. and Welsshaar,B.
A pipeline for automated high-throughput generation of FSTs (flanking sequence tags) from Arabidopsis thaliana T-DNA transformed lines thale cress. Arabidopsis thaliana Arabidopsis, Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; Spermatophyta; Magnoliophyta; eudicotyledons; care eudicots; Rosidae; eurosids II; Brassicales; Brassicaceae; Arabidopsis. ROSSO,M., Strizhov,N., Li,Y., Reiss,B., Dekker,K: and Weisshaar,B. A new Arabidopsis thaliana T-DNA mutagenised population (GABI-Kat) for flanking sequence tag based reverse genetics Unpublished AL762543 AL762543.1 GI:21508636 Arabidopsis thaliana T-DNA flanking sequence GK-025G03-013722, ALTASSA 2 Unpublished GSS. (bases 1 to 176) Max-Planck-Institut

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Submitted (17-JUN-2002) Weisshaar
                                                                                                      Rosso,M., Strizhov,N., Li,Y., Reiss,B., Dekker,K. and Weisshaar,B. A new Arabidopsis thaliana T-DNA mutagenised population (GABI-Kat) for flanking sequence tag based reverse genetics
                                                                                                                                                                                                                                                                                                                                                        Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; Rosidae; eurosids II; Brassicales; Brassicaceae; Arabidopsis.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Arabidopsis thaliana T-DNA flanking sequence genomic survey sequence.
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                    Direct Submission
                                                                                        Unpublished
                                                                                                                                                                                                                                                                                              and Weisshaar, B
                                                                                                                                                                                                                                                                                                                Strizhov, N., Li, Y., Rosso, M., Viehoever, P., Dekker, K., Saedler, H
                                                                                                                                                                                                                                                                                                                                                                                                                              Arabidopsis thaliana
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                                                                                                                                                                                                                                             A pipeline for automated high-throughput generation of FSTs (flanking sequence tags) from Arabidopsis thaliana T-DNA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              /notes "PCR was performed on DNA from Arabidopsis thalia plants (T1) which were transformed with the T-DNA from vector pAC106. The lines contain one or more T-DNA insertions. The DNA fragment(s) resulting from the PCR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            processed for submission. T-DNA derived sequences
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COMMENT

Email: mseki@rtc.riken.go.jp An Arabidopsis full-length cDNA library was constructed essentially as reported previously (Seki et al., 1998). This clone is in a

RIKEN Genomic Sciences Center
3-1-1 Koyadai, Tsukuba, Ibaraki 305-0074,
Tel: 81-298-36-4359
Fax: 81-298-36-9060

Plant Functional Genomics Research Group

Contact: Motoaki Seki

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Best Local
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                                        Seki,M., Narusaka,M., Ishida,J., Kamiya,A., Satou,M., Nakajima,M., Oono,Y., Sakurai,T., Carninci,P., Kawai,J., Itoh,M., Ishii,Y., Arakawa,T., Shibata,K., Shinagawa,A., Muramatsu,M., Hayashizaki,Y. and Shinozaki,K.
                                                                                                                                       Arabidopsis thaliana
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
Rosidae; eurosids II; Brassicales; Brassicaceae; Arabidopsis.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Zuechtungsforschung, Carl-von-Linne-Weg 10, Koeln, 50829, Germa This sequence is recovered from the left border of the T-DNA. I indicates an insertion within the locus defined by clone T3A5. sequences are generated at the MPI for Plant Breeding Research the context of the GABI-Kat project. GABI-Kat is part of the Ge Plant Genomics program designated 'GABI'. Information on line availability can be found at:

http://www.mpiz-koeln.mpg.de/GABI-Kat/.
                                                                                                                                                                                                                                                                                    mRNA sequence.
AV787618
                                                                                                                                                                                                                                                                                                                          AV787618 RAFL6 Arabidopsis thaliana
Unpublished (2002)
                  Large scale analysis of Arabidopsis full-length cDNA (2002b)
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a 37 c
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/note="PCR was performed on DNA from Arabidopsis thaliana
plants (T1) which were transformed with the T-DNA from
vector pAC106. The lines contain one or more T-DNA
insertions. The DNA fragment(s) resulting from the PCR
were directly sequenced to determine the genomic sequence
flanking the insertion. Sequences displaying significant
similarity to the A. thalalan nuclear genome sequence were
processed for submission. T-DNA derived sequences were
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     /strain="Columbia 0"
/db_xref="taxon:3702"
/clone="GK-025G03-013757"
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98.6%;
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Pred. No. 2.
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he T-DNA. It
lone T3A5. The
g Research in
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FEATURES

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Determination of this BAC-end sequence was carried out as part of a collaboration with the Berkeley Drosophila Genome Project (BDGP). The BDGP is constructing a physical map of the Drosophila please see http://www.fruitfly.org The BDGP Drosophila please see http://www.fruitfly.org The BDGP Drosophila melanogaster BAC library was prepared by Kazutoyo Osoegawa and Cancer Genetics at the Roswell Park Cancer Institute in Buffalo, NY. The library is named RPCI-98 and was constructed by partial isogenic strain y2; on bw sp. the same strain used for the BDGP's and how to order individual BAC clones, the entire library, or filters for hybridization from the BACPAC Resource Center can be found at http://bacpac.med.buffalo.edu/drosophila_bac.htm.
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Drosophila melanogaster
Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;
Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha;
Ephydroidea; Drosophilidae; Drosophila.
                                                                                                                                                                                                                                                                                                                                                                                     Submitted (11-JUN-1999) Genoscope - Centre National de Sequencage : BP 191 91006 EVRY cedex - FRANCE (E-mail : seqref@genoscope.cns.fr
                                                                                                                                                                                                                                                                                                                                                                                                                                                     Genoscope.
Direct Submission
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AL078714
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             ∕organism="Drosophila melanogaster"
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/lab_host="DH10B"
/note="Site_1: SSII; Site_2: xhoI; subjected to dehydration (1, 2, 5, 10, 24 hr) and cold (1, 2, 5, hr) treatments"

79 c 64 g 124 t
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/db_xref="taxon:3702"
/clone="RAFL06-76-F19"
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                                                                            source
                                                                                                - Web: www.genoscope.cns.fr)
Determination of this BAC-end sequence was carried out as part of a collaboration with the Berkeley Drosophila Genome Project (BDGP). The BDGP is constructing a physical map of the Drosophila please see http://www.fruitfly.org The BDGP Drosophila please for pleter de Jong's laboratory in the Department of Cancer Genetics at the Roswell Park Cancer Institute in Buffalo, Ecori digestion of Drosophila DNA provided by the BDGP from the library is named RPCI-98 and was constructed by partial isogenic strain y2; on bw sp, the same strain used for the BDGP's and how to order individual BAC clones, the entire library, or filters for hybridization from the BACPAC Resource Center can be found at http://bacpac.med.huffalo.edu/drosophila bac.htm
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                                                                                         found at http://bacpac.med.buffalo.edu/drosophila_bac.htm
                                                                                                                                                                                                                                                                                                                                                                                                             Submitted (02-JUN-1999) Genoscope - Centre National de Sequencage BP 191 91006 EVRY cedex - FRANCE (E-mail : seqref@genoscope.cns.fr
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Drosophila melanogaster.
Drosophila melanogaster
Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;
Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha;
Ephydroidea; Drosophilidae; Drosophila.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Direct Submission
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BACR27A24 of RPCI-98 library from
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/organism="Drosophila melanogaster"
/db_xref="taxon:7227"
/clone="BACR27A24"
                                                                                     Location/Qualifiers
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/clone="BACR48P19"
/clone=lib="RPC1-98"
/note="end: TET3"
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                                                                                                                     Determination of this BAC-end sequence was carried out as part of a collaboration with the Berkeley Drosophila Genome Project (BDGP). The BDGP is constructing a physical map of the Drosophila melanogaster genome using these BACs. For further information please see http://www.fruitfly.org The BDGP Drosophila melanogaster BAC library was prepared by Kazutoyo Osoegawa and Aaron Mammoser in Pleter de Jong's laboratory in the Department of Cancer Genetics at the Roswell Park Cancer Institute in Buffalo, NY. The library is named RPCI-98 and was constructed by partial EcoRI digestion of Drosophila DNA provided by the BDGP from the isogenic strain y2; on bw sp, the same strain used for the BDGP's pland EST libraries. A more detailed description of the library
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                                                                                                                                                                                                                                                                                                                        BP 191
                                                                                                                                                                                                                                                                                                                                  Submitted (02-JUN-1999) Genoscope - Centre National de Sequencage BP 191 91006 EVRY cedex - FRANCE (E-mail : seqref@genoscope.cns.fi
                                                                                                                                                                                                                                                                                                                                                                                                                Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota; Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha; Ephydroidea; Drosophilidae; Drosophila.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               fly), genomic survey sequence. AL077798 AL077798.1 GI:4957174
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                                                         and how to order individual BAC clones, the entire library, or filters for hybridization from the BACPAC Resource Center can be found at http://bacpac.med.buffalo.edu/drosophila_bac.htm.
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/db_xref="taxon:72
/clone="BACR17N06"
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                   This sequence is a single read and was generated as part of a scale clone-end sequencing project of the Tetraodon nigrovirid genome. For more information, please take a look at http://www.genoscope.cns.fr/Tetraodon.
                                                                                                                                                                                                                                                                                                                                                                                                    Tetraodontidae; Tetraodon.

1 (bases 1 to 1027)

Roest-Crollius,H., Jaillon,O., Dasilva,C., Bouneau,L., Fisher,C.,
Bernot,A., Fizames,C., Wincker,P., Brottler,P., Quetler,F.,
Saurin,W. and Weissenbach,J.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       GSS; genome survey sequence. Tetraodon nigroviridis. Tetraodon nigroviridis
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Roest-Crollius, H., Jaille
Bouneau, L., Billault, A.,
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Tetraodon nigroviridis genome survey sequence T7 end of c
163Ml6 of library G from Tetraodon nigroviridis, genomic
                                                                                                         Submitted (12-APR-2000)
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                                                                                                                                                                                         Unpublished
                                                                                                                                                                                                                                                         Weissenbach,J.
                                                                                                                                                                                                                                                                                                                                        Unpublished
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lt,A., Quetier,F., Saurin,W., Bernot,A. and
                                                                                                                                                                                                           repeat analysis of the compact genome of the sh Tetraodon nigroviridis
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Determination of this BAC-end sequence was carried out as part of a collaboration with the European Drosophila Genome Project (EDGP) - http://www.edgp.ebi.ac.uk - This Drosophila melanogaster BAC library (Dros BAC) was made by Alain Billaud at CEPH (Centred European Constructed du Polymorphisme Humain) with funding provided by a MRC project grant. The DNA was prepared from embryos by Alain Bucheton and Genevieve Payan. It has been constructed in the vector
                                                                                                                Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                 Submitted (23-JUL-1999) Genoscope - Centre National de Sequencage :
BP 191 91006 EVRY cedex - FRANCE (E-mail : seqref@genoscope.cns.fr
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Drosophila melanogaster
Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;
Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha;
Ephydroidea; Drosophilidae; Drosophila
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                                                                                                                                                                                      /plasmid="pBeloBAC11"
/note="end : T7"
                                                                                                                                                                                                                 /organism="Drosophila melanogaster"
/db_xref="taxon:7227"
/clone="%BCRNIAGD2"
/clone_lib="DrosBAC"
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1. .1101
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/clone_lib="G"
/note="Genoscope sequence ID : COAG163BG08LP1~end : T7"
86 c 100 g 381 t 130 others
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/db_xref="taxon:99883"
/clone="163M16"
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                                                                                             16.2%; Score 58; J
34.3%; Pred. No. 3
tive 76; Mismatch
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High quality sequence stop: 291
Location/Qualiflers
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Fax: 301 838 3543
Email: bjloftus@tigr.org
Clones are derived from the
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Department of Eukaryotic Genomics
The Institute for Genomic Research
9712 Medical Center Dr., Rockville,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Class: shotgun
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Entamoeba histolytica
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                                                            /Clone_1ib="Entamoba histolytica Sheared DNA"
/note="Vector: pHOS1; Site_1: Bst I; Constructed at The
Institute for Genomic Research (TIGR), Rockville, MD.
Genomic DNA isolated from broth cultures of E. histolytica
using a method described by Clark and Diamond (Clark,
C.G., and Diamond, L.S. (1993) Entamoba histolytica: a
method for isolate identification. Exp. Parasitol.
Tight size distribution (~2 kb). The v + i method used for
the library construction is described in detail in Smith,
whole genome shotgun sequencing projects. In Genome
Sequencing: A Practical Approach, eds. M. Vaudin and B.
Barell, Oxford University Press, 1999)."
                                                                                                                                                                                                                                                                                                                                               /organism="Entamoeba histolytica"
/strain="HM1: IMSS"
/db_xref="taxon: 5759"
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     16.18;
64.78;
 Score 57.8;
Pred. No. 3.
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Best Local
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                                                                                                                                                                   Determination of this BAC-end sequence was carried out as part of a collaboration with the Berkeley Drosophila Genome Project (BDGP). The BDGP is constructing a physical map of the Drosophila melanogaster genome using these BACs. For further information please see http://www.fruitfly.org The BDGP Drosophila melanogaster BAC library was prepared by Kazutoyo Osoegawa and Aaron Mammoser in Pieter de Jong's laboratory in the Department of Cancer Genetics at the Roswell Park Cancer Institute in Buffalo, NY. The library is named RPCI-98 and was constructed by partial EcoRI digestion of Drosophila DNA provided by the BDGP from the isogenic strain y2; cn bw sp, the same strain used for the BDGP's pl and EST libraries. A more detailed description of the library
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                                                                                TTTTTTTTGCCCAATGATATATAAAATTTGGATAAATATATTATTGGATATTCGTTTT 120
                                                                                                                           TTAGTTCGGGTTT 133
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BACR29K22 of RPCI-98 library from Drosophila melanogaster
                                                                                                                                                                                                                                                                                                                                                                                                                                                                          and how to order individual BAC clones, the entire library, or filters for hybridization from the BACPAC Resource Center can be found at http://bacpac.med.buffalo.edu/drosophila_bac.htm.
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/note="end : T7"
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/db_xref="taxon:7227"
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42.1%;
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survey sequence T7 end of BAC:
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                                                                                                   AGGGTTTCGACTTTCGAAAGTGGACGATGTATATAGATTGGGAGCTAGGTTGAGTCTTTG 199
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             - Web: www.genoscope.cns.fr)

Determination of this BAC-end sequence was carried out as part of a collaboration with the European Drosophila Genome Project (EDGP) - http://www.edgp.ebi.ac.uk - This Drosophila melanogaster BAC library (Dros BAC) was made by Alain Billaud at CEPH (Centre d'Etude du Polymorphisme Humain) with funding provided by a MRC project grant. The DNA was prepared from embryos by Alain Bucheton and Genevieve Payan. It has been constructed in the vector
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Drosophila melanogaster
Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;
Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha;
Ephydroidea; Drosophilidae; Drosophila.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 fly), genomic survey sequence. AL109126
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   CNS018BG 894 bp DNA linear GSS 26-JUL-1999 Drosophila melanogaster genome survey sequence T7 end of BAC BACN13B16 of DrosBAC library from Drosophila melanogaster (fruit
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Submitted (23-JUL-1999) Genoscope - Centre National de Sequencage : BP 191 91006 EVRY cedex - FRANCE (E-mail : seqref@genoscope.cns.fr
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/note="end : T7"
101 c 85 g
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/db_xref="taxon:7227"
/clone="BACN13B16"
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AL Submitted (08-5EP-2000) Genoscope - Centre National de Sequencage, 2 rue Gaston Cremieux, CP 5706, 91057 EVRY cedex, FRANCE. (E-mail: seqref@genoscope.cns.fr - Web: www.genoscope.cns.fr)
This GSS is part of a random genomic sequencing program of thirteen yeast species: Saccharomyces bayanus var. uvarum, Saccharomyces exiguus, Saccharomyces servazzii, Zyoosaccharomyces rouxii, Saccharomyces kluyveri, Kluyveromyces thermotolerans, Kluyveromyces lactis var. lactis, Kluyveromyces thermotolerans, Kluyveromyces angusta, Debaryomyces hansenii var. hansenii, Pichia sorbitophila, Candida tropicalis and Yarrowia lipolytica. Genomic inserts of 3 to keywords for description of this sequence and for the sequence of the other extremity of this insert.
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FBBS Lett. 487 (1), 3-12 (2000)
                                                                                         Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Kluyveromyces lactis
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Bolotin-Fukuhara,M., Toffano-Nioche,C., Artiguenave,F., Duchateau-Nguyen,G., Lemaire,M., Marmeisse,R., Montrocher,R., Robert,C., Termiter,M., Wincker,P. and Wesolowski-Louvel,M. Genomic exploration of the hemiascomycetous yeasts: 11.
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Eukaryota; Fungi; Ascomycota; Saccharomycotina; Saccharomycetes;
Saccharomycetales; Saccharomycetaceae; Kluyveromyces.

1 (bases 1 to 1147)
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/clone="BA0AB018F06"
/clone_11b="BA0AB"
/clone_11b="BA0AB"
a 120 c 175 g 3
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                                                                                                                                                                                                                                                                                  /organism="Kluyveromyces
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      70 CCCAATGATATAAAAAATTTGGATAAATAATATTATTGGATATTCGTTTTTTAGTTCGG 129
                                                                           TTTTTGMATTWWWTTTKNTDAGTAAWWAATTTTTWATAATTTTTTKRTTTTTTTTTTT
                                                                                                   TTTTTTTGCCCAATGATATATAAAAATTTGGATAAATAATATTATTGGATATTCGTTTTT
TTTTTTTATTWATGAARTTTTTTTTTTTTTKAAAARGGAWTTADAAAWTTAAA 1066
                                                                                                                                                                                     TTTTTTTTTTTAKTTKGGGGGRRTTTTKTKKKKKGGGKKKKAWGA 911
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  TGAGTCTTTGGACATTTGTATTGGATGTTGTTGATTATTAGTGTCGA 236
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        RATAWAAAAWWAAAGWAKAGTDWWWAAAAATAGRTTWWWWWTAATAAATKWRWTDGGKGT 864
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               GTTTGAGAAAAGGGTTTCGACTTTCGAAAGTGGAGCGATGTATATAGATTGGGAGCTAGGT 189
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 TTTTTTTTTTTTTTATATATWAWWAAAAAWTWARAWAAGATAATTTTTTTTTKTKGGGR 804
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Submitted (23-UIL-1999) Genoscope - Centre National de Sequencage: BP 191 91006 EVRY cedex - FRANCE (E-mail: seqref@genoscope.cns.fr )

Www.genoscope.cns.fr)

Determination of this BAC-end sequence was carried out as part of a collaboration with the European Drosophila Genome Project (EDGP) - http://www.edgp.ebi.ac.uk - This Drosophila melanogaster BAC library (Dros BAC) was made by Alain Billaud at CEPH (Centre d'Etude du Polymorphisme Humain) with funding provided by a MRC project grant. The DNA was prepared from embryos by Alain Bucheton and Genevieve Payan. It has been constructed in the vector
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Drosophila melanogaster
Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;
Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha;
Ephydroidea; Drosophilidae; Drosophila.
1 (bases 1 to 1101)
                                                                                                                                                                                                                                                            Similarity
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AL097397
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Drosophila melanogaster genome survey sequence T7 end of BAC BACN01C10 of DrosBAC library from Drosophila melanogaster (fruit
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Direct Submission
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                AL097397.1 GI:5609008
                                                                                                                                                                                                                                                                                                                                         254
                                                                                                                                                                                                                                         Conservative
                                                                                                                                                                                                                                                                                                                                                                                      /organism="Drosophila melanogaster"
/db_xref="taxon:7227"
/clone="BACN01C10"
/clone_lib="Drosbac"
                                                                                                                                                                                                                                                                                                                                   /plasmid="pBeloBAC11"
/note="end : T7"
288 c 267 g
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ocation/Qualifiers
                                                                                                                                                                                                                                                            15.8%;
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                                                                                                                                                                                                                                       24;
                                                                                                                                                                                                                                                          Score 56.4;
Pred. No. 5
                                                                                                                                                                                                                                     Mismatches
                                                                                                                                                                                                                                                                                                                                   177
                                                                                                                                                                                                                                                                          DB
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 573
                                                                             633
                                                                                                                                                                                                                                                                                                          813
                                                                                                                                                                                                                                                                                                                                                                                  300 CAACTTTTACTTCGTTTTTGATCCGAAGCAATAACAAATTGTCAAATACCAAA 352
                                                                                                              240
                                                                                                                                                        693
                                                                                                                                                                                          181
                                                                                                                                                                                                                               753
                                                                                                                                                                                                                                                                     121
                                                                                                                                                                                                                                                                                                                                                61
                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Determination of this BAC-end sequence was carried out as part of a bollaboration with the Berkeley Drosophila Genome Project (BDGP). The BDGP is constructing a physical map of the Drosophila melanogaster genome using these BACs. For further information please see http://www.fruitfly.org The BDGP Drosophila melanogaster BAC library was prepared by Kazutoyo Osoegawa and Aaron Mammoser in Pleater de Jong's laboratory in the Department of Cancer Genetics at the Roswell Park Cancer Institute in Buffalo, NY. The library is named RPCI-98 and was constructed by partial EcoRI digestion of Drosophila DNA provided by the BDGP from the 1sogenic strain y2; cn bw sp. the same strain used for the BDGP's Pl and EST libraries. A more detailed description of the library and how to order individual BAC clones, the entire library, or filters for hybridization from the BACPAC Resource Center can be Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                     GAGCTAGGTTGAGTCTTTGGACATTTGTAT-TGGATGTTGATTAGTGTCGACAC
                                                                                                                                                                                                                             TATTAAACCTTAAATGGGCTTTCTATAAGGCCCAATTATATTACGATTATAACAAAGTGA
                                                                                                                                                                                                                                                                                                        AAAATTAAAATTAAWAAAAAAAAAAAAAAAAAAWTAATTAAWAAAAAWTAA
                                                                         TTAGTTCGGGTTTGAGAAAAGGGTTTCGACTTTCGAAAGTGGACGATGTATATAGATTGG
                                                                                                                                                                                                                                                                                                                                            TTTTTTTGCCCCAATGATATATAAAAATTTGGATAATAATATTATTGGATATTCGTTTT 120
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 CNS0021J 1101 bp DNA linear GSS 03-JUN-1999 Drosophila melanogaster genome survey sequence TET3 end of BAC #BACR05N11 of RPCI-98 library from Drosophila melanogaster (fruit
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Submitted (02-JUN-1999) Genoscope - Centre National de Sequencage : BP 191 91006 EVRY cedex - FRANCE (E-mail : seqref@genoscope.cns.fr
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Drosophila melanogaster
Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;
Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha;
Ephydroidea; Drosophilidae; Drosophila.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Direct Submission
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          631
                                                                                                                                                                                                                                                                                                                                                                                                                                                               Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          נם
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             /organism="Drosophila melanogaster"
/db_xref="taxon:7227"
/clone="BACR05N11"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            /note="end :
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               clone_lib="RPCI-98"
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28 g
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Pred. No. 6.1;
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RESULT 15

Search completed: March 30, Job time: 474.144 secs

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Best Local
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                                                                                                                                820
700
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                             124 GTTCGGGTTTGAGAAAAGGGTTTCGACTTT 153
                                                                                              64
                                                                                                                                              TTTTTGCCCCAATGATATATAAAAATTTGGATAAATAATATTATTGGATATTCGTTTTTTA 123
                                                                                                                            This sequence is a single read and was generated as scale clone-end sequencing project of the Tetraodon genome. For more information, please take a look at http://www.genoscope.cns.fr/Tetraodon.
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1 (bases 1 to 949)

Roest-Crollius H., Jaillon,O., Dasilva,C., Bouneau,L.,
Bernot,A., Fizames,C., Wincker,P., Brottier,P., Quetie,
Saurin,W. and Weissenbach,J.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      AL281906.1 GI:8020236
GSS; genome survey sequence.
Tetraodon nigroviridis.
Tetraodon nigroviridis
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949 bp DNA linear GSS 21-MAY-:
Tetraodon nigroviridis genome survey sequence T7 end of clone
095F19 of library G from Tetraodon nigroviridis, genomic survey
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Charaterization and repeat analysis of the compact genome of the freshwater pufferfish Tetraodon nigroviridis
                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Submitted (12-APR-2000)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Unpublished
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Weissenbach,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Bouneau, L., Billault, A.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Unpublished
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Human gene number estimate
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Actinopterygii; Neopterygii; Teleostei; Euteleostei; Neoteleostei; Acanthomorpha; Acanthopterygii; Percomorpha; Tetraodontiformes;
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                                                                                                                                                                                                               Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              (bases 1 to 949)
                                                                                                                                                                                                                                                                                355
                                                                                                                                                                                               Conservative
                                                                                                                                                                                                                                                                                                                          /organism="Tetraodon nigroviridis"
/db_xref="taxon:99883"
/clone="095F19"
                                                                                                                                                                                                                                                                            /clone_11b="G"
/note="Genoscope sequence ID : C0BG095CC10LP1-end : T7"
144 c    185 g    223 t    42 others
                                                                                                                                                                                                             15.6%;
                                                                                                                                                                                             21;
                                                                                                                                                                                                         Score 56; Pred. No. 7
                                                                                                                                                                                             Mismatches
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Quetier,F., Saurin,W.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          provided by genome wide analysis using sequence
                                                                                                                                                                                                                            DB 17;
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Quetier,F.,
                                                                                                                                                                                                                                                                                                                                                                                                                                           part of a large nigroviridis
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d of clone
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